Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	5098	(magnetic near2 field) same array	USPAT; EPO; DERWENT	OR	OFF	2005/01/13 15:38
L2	682	(magnetic near2 field) same array same sensor	USPAT; EPO; DERWENT	OR	OFF	2005/01/13 15:38
L3	2	l2 same (DNA or RNA or protein or peptide or antibody)	USPAT; EPO; DERWENT	OR	OFF	2005/01/13 15:38

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                   STN Express with Discover!
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 NEWS  7  DEC 09   12 databases to be removed from STN on December 31, 2004
 NEWS  8  DEC 15   MEDLINE update schedule for December 2004
 NEWS  9  DEC 17   ELCOM reloaded; updating to resume; current-awareness
                   alerts (SDIs) affected
 NEWS  10 DEC 17   COMPUAB reloaded; updating to resume; current-awareness
                   alerts (SDIs) affected
 NEWS  11 DEC 17   SOLIDSTATE reloaded; updating to resume; current-awareness
                   alerts (SDIs) affected
 NEWS  12 DEC 17   CERAB reloaded; updating to resume; current-awareness
                   alerts (SDIs) affected
 NEWS  13 DEC 17   THREE NEW FIELDS ADDED TO IFIPAT/IFIUDB/IFICDB
 NEWS  14 DEC 30   EPFULL: New patent full text database to be available on STN
 NEWS  15 DEC 30   CAPLUS - PATENT COVERAGE EXPANDED
 NEWS  16 JAN 03   No connect-hour charges in EPFULL during January and
                   February 2005
 NEWS  17 JAN 11   CA/CAPLUS - Expanded patent coverage to include Russia
                   (Federal Institute of Industrial Property)

 NEWS EXPRESS  JANUARY 10 CURRENT WINDOWS VERSION IS V7.01a, CURRENT
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               AND CURRENT DISCOVER FILE IS DATED 10 JANUARY 2005

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accessing the remaining file names entered.
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'IGNORE\' IS NOT A VALID FILE NAME
Enter "HELP FILE NAMES" at an arrow prompt (=>) for a list of files
that are available.  If you have requested multiple files, you can
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accessing the remaining file names entered.
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=> (swing or spatial or remant or coercive or magnitude) and (magnetic or
magnetism) and (target or DNA or RNA or protein or peptide) and (binding or bind or
bound)
L1           2 FILE AGRICOLA
L2         158 FILE BIOTECHNO
L3           0 FILE CONFSCI
L4           0 FILE HEALSAFE
L5           0 FILE IMSDRUGCONF
L6          36 FILE LIFESCI
L7           0 FILE MEDICONF
L8          62 FILE PASCAL

TOTAL FOR ALL FILES
L9         258 (SWING OR SPATIAL OR REMANT OR COERCIVE OR MAGNITUDE) AND (MAGNE
               TIC OR MAGNETISM) AND (TARGET OR DNA OR RNA OR PROTEIN OR PEPTID
               E) AND (BINDING OR BIND OR BOUND)

=> l9 and probe
L10          0 FILE AGRICOLA
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L11          15 FILE BIOTECHNO
L12           0 FILE CONFSCI
L13           0 FILE HEALSAFE
L14           0 FILE IMSDRUGCONF
L15           6 FILE LIFESCI
L16           0 FILE MEDICONF
L17           1 FILE PASCAL

TOTAL FOR ALL FILES
L18          22 L9 AND PROBE

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ENTER L# LIST OR (END):l18
DUPLICATE IS NOT AVAILABLE IN 'IMSDRUGCONF, MEDICONF'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L18
L19           20 DUP REM L18 (2 DUPLICATES REMOVED)

=> d l19 ibib abs total

L19   ANSWER 1 OF 20  BIOTECHNO  COPYRIGHT 2005 Elsevier Science B.V. on STN
      DUPLICATE
ACCESSION NUMBER:         2003:37221389   BIOTECHNO
TITLE:                    Nanoparticle-based bio-bar codes for the
                          ultrasensitive detection of proteins
AUTHOR:                   Nam J.-M.; Thaxton C.S.; Mirkin C.A.
CORPORATE SOURCE:         C.A. Mirkin, Department of Chemistry, Institute for
                          Nanotechnology, Northwestern University, 2145 Sheridan
                          Road, Evanston, IL 60201, United States.
                          E-mail: camirkin@chem.northwestern.edu
SOURCE:                   Science, (26 SEP 2003), 301/5641 (1884-1886), 27
                          reference(s)
                          CODEN: SCIEAS  ISSN: 0036-8075
DOCUMENT TYPE:            Journal; Article
COUNTRY:                  United States
LANGUAGE:                 English
SUMMARY LANGUAGE:         English
AN    2003:37221389   BIOTECHNO
AB    An ultrasensitive method for detecting protein analytes has
      been developed. The system relies on magnetic microparticle
      probes with antibodies that specifically bind a
      target of interest [prostate-specific antigen (PSA) in this case]
      and nanoparticle probes that are encoded with DNA
      that is unique to the protein target of interest and
      antibodies that can sandwich the target captured by the
      microparticle probes. Magnetic separation of the
      complexed probes and target followed by
      dehybridization of the oligonucleotides on the nanoparticle probe
      surface allows the determination of the presence of the target
      protein by identifying the oligonucleotide sequence released from
      the nanoparticle probe. Because the nanoparticle probe
      carries with it a large number of oligonucleotides per protein
      binding event, there is substantial amplification and PSA can be
      detected at 30 attomolar concentration. Alternatively, a polymerase chain
      reaction on the oligonucleotide bar codes can boost the sensitivity to 3
      attomolar. Comparable clinically accepted conventional assays for
      detecting the same target have sensitivity limits of .apprx.3
      picomdar, six orders of magnitude less sensitive than what is
      observed with this method.

L19   ANSWER 2 OF 20  BIOTECHNO  COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER:         2002:34292998   BIOTECHNO
TITLE:                    Synthesis of new transglycosidically tethered
                          5'-nucleotides constrained to a highly biologically
```

relevant profile
AUTHOR: Groziak M.P.; Thomas D.W.
CORPORATE SOURCE: M.P. Groziak, SRI International, 333 Ravenswood Ave., Menlo Park, CA 94025-3493, United States.
E-mail: michael.groziak@sri.com
SOURCE: Journal of Organic Chemistry, (05 APR 2002), 67/7 (2152-2159), 62 reference(s)
CODEN: JOCEAH ISSN: 0022-3263
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2002:34292998 BIOTECHNO
AB A new motif for restricting 5'-nucleotides to highly biologically relevant conformations has been developed. The 5',6-oxomethylene transglycosidically tethered versions of uridine 5'-monophosphate and 2'-deoxyuridine 5'-monophosphate (1 and 2, respectively) were synthesized in 10-11 steps from their respective natural nucleoside precursors along routes general to the preparation of tethered versions of a wide variety of 5'-nucleotide-based compounds. In both routes, a shelf-stable 6-hydroxymethyl pyrimidine nucleoside 5'-carboxaldehyde is the key intermediate. It exists in a carbohydrate-like fashion in a cyclic hemiacetal form under aprotic conditions. The phosphorylated cyclic hemiacetals 1 and 2 were isolated as binary mixtures of 5'-diastereomers differing principally in the trajectory of the phosphate group with respect to the carbohydrate. By .sup.1H NMR, both 1 and 2 were demonstrated to be stable to hydrolysis at ambient temperature in D.sub.20 solution for at least 2 months. The oxomethylene transglycosidic tether as deployed in 1 and 2 leaves all of the native 5'-nucleotide molecular recognition Sites intact while it restricts the framework to a low-energy anti glycosyl conformation and an extended phosphate disposition. This provides a **spatial** presence that approximates nearly three-quarters of the **protein-bound** 5'-nucleotide ligands described in the **Protein** Data Bank. The tether has a low structural and electronic impact, occupies a region of space (over the β-face of the furan ring) seldom penetrated by **proteins**, and should be accommodated as readily on purine-based 5'-nucleotide frameworks as on pyrimidine-based ones. Because of its unique and attractive features, this new motif for the conformational restriction of 5'-nucleotides is expected to be useful for producing **probes** of structure/function relationships and in assessing the conformational **binding** requirements that enzymes and receptor sites have for their natural 5'-nucleotide-based ligands.

L19 ANSWER 3 OF 20 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 2002:35463420 BIOTECHNO
TITLE: Role of proline, cysteine and a disulphide bridge in the structure and activity of the anti-microbial **peptide** gaegurin 5
AUTHOR: Park S.-H.; Kim H.-E.; Kim C.-M.; Yun H.-J.; Choi E.-C.; Lee B.-J.
CORPORATE SOURCE: B.-J. Lee, Res. Inst. of Pharmaceutical Sci., College of Pharmacy, Seoul National University, Seoul 151-742, South Korea.
E-mail: Ibj@nmr.snu.ac.kr
SOURCE: Biochemical Journal, (15 NOV 2002), 368/1 (171-182), 51 reference(s)
CODEN: BIJOAK ISSN: 0264-6021
DOCUMENT TYPE: Journal; Article
COUNTRY: United Kingdom
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2002:35463420 BIOTECHNO
AB Gaegurin 5 (GGN5) is a cationic 24-residue anti-microbial **peptide**

isolated from the skin of a Korean frog, Rana rugosa. It contains a central proline residue and an intra-residue disulphide bridge in its C-terminus, which are common to the anti-microbial **peptides** found in Ranidae. We determined the solution structure of GGN5 **bound** to SDS micelles for the first time and investigated the role of proline, cysteine and a disulphide bridge on the structure and activity of GGN5. GGN5 adopts an amphipathic α-helical structure spanning residues 3-20 kinked around Pro-14, which allows the hydrophobic residues to reside in the concave helical region, and a disulphide-bridged loop-like conformation in its C-terminus. By replacement of proline with alanine (.sup.P.sup.AGGN5), a straight and rigid helix was formed in the central region and was more stable than the kinked helix. Reduction of a disulphide bridge in the C-terminus (GGN5.sup.S.sup.H) maintained the loosely ordered loop-like conformation, while the replacement of two cysteines with serines (.sup.C.sup.SGGN5) caused the C-terminal conformation to be completely disordered. The **magnitude** of anti-microbial activity of the **peptides** was closely related to their helical stability in the order .sup.P.sup.AGGN5 > GGN5 > GGN5.sup.S.sup.H > .sup.C.sup.SGGN5, suggesting that the helical stability of the **peptides** is important for anti-microbial activity. On the other hand, the significant increase of haemolytic activity of .sup.P.sup.AGGN5 implies that a helical kink of GGN5 could be involved in the selectivity of **target** cells. The location of GGN5 and .sup.P.sup.AGGN5, analysed using paramagnetic **probes**, was mainly at the surface of SDS micelles, although the location of the N-terminal region was slightly different between them.

L19 ANSWER 4 OF 20 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 2002:35414676 BIOTECHNO
TITLE: Observation of H-bond mediated .sup.3.sup.hJ.sub.H.sub.2.sub.H.sub.3 coupling constants across Watson-Crick AU base pairs in **RNA**
AUTHOR: Luy B.; Richter U.; DeJong E.S.; Sorensen O.W.; Marino J.P.
CORPORATE SOURCE: J.P. Marino, Center for Adv. Res. in Biotech., Univ. of Maryland Biotechnol. Inst., National Inst. of Standards/Technol., 9600 Gudelsky Dr., Rockville, MD 20850, United States.
E-mail: marino@carb.nist.gov
SOURCE: Journal of Biomolecular NMR, (01 OCT 2002), 24/2 (133-142), 65 reference(s)
CODEN: JBNME0 ISSN: 0925-2738
DOCUMENT TYPE: Journal; General Review
COUNTRY: Netherlands
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2002:35414676 BIOTECHNO
AB .sup.3.sup.hJ.sub.H.sub.2.sub.H.sub.3 trans-hydrogen bond scalar coupling constants have been observed for the first time in Watson-Crick AU base pairs in uniformly .sup.1.sup.5N-labeled **RNA** oligonucleotides using a new .sup.2.sup.hJ.sub.N.sub.N-HNN-E. COSY experiment. The experiment utilizes adenosine H2 (AH2) for original polarization and detection, while employing .sup.2.sup.hJ.sub.N.sub.N couplings for coherence transfer across the hydrogen bonds (H-bonds). The H3 protons of uracil bases are unperturbed throughout the experiment so that these protons appear as passive spins in E. COSY patterns. .sup.3.sup.hJ.sub.H.sub.2.sub.H.sub.3 coupling constants can therefore be accurately measured in the acquisition dimension from the displacement of the E. COSY multiplet components, which are separated by the relatively large .sup.1J.sub.H.sub.3.sub.N.sub.3 coupling constants in the indirect dimension of the two-dimensional experiment. The .sup.3.sup.hJH2H3 scalar coupling constants determined for AU base pairs in the two **RNA** hairpins examined here have been found to be positive and range in

magnitude up to 1.8 Hz. Using a molecular fragment representation of an AU base pair, density functional theory/finite field perturbation theory (DFT/FPT) methods have been applied to attempt to predict the relative contributions of H-bond length and angular geometry to the **magnitude** of .sup.3.sup.hJ.sub.H.sub.2.sub.H.sub.3 coupling constants. Although the DFT/FPT calculations did not reproduce the full range of **magnitude** observed experimentally for the .sup.3.sup.hJ.sub.H.sub.2.sub.H.sub.3 coupling constants, the calculations do predict the correct sign and general trends in variation in size of these coupling constants. The calculations suggest that the **magnitude** of the coupling constants depends largely on H-bond length, but can also vary with differences in base pair geometry. The dependency of the .sup.3.sup.hJ.sub.H.sub.2.sub.H.sub.3 coupling constant on H-bond strength and geometry makes it a new **probe** for defining base pairs in NMR studies of nucleic acids.

L19 ANSWER 5 OF 20 LIFESCI COPYRIGHT 2005 CSA on STN
ACCESSION NUMBER: 2001:98980 LIFESCI
TITLE: Backbone Dynamics of Receptor **Binding** and Antigenic Regions of a Pseudomonas aeruginosa Pilin Monomer
AUTHOR: Suh, Jeong-Yong; Spyracopoulos, L.; Keizer, D.W.; Irvin, R.T.; Sykes, B.D.
CORPORATE SOURCE: PENCE, 713 Heritage Medical Research Center, Edmonton, Alberta, T6G 2S2, Canada; E-mail: brian.sykes@ualberta.ca
SOURCE: Biochemistry (Washington) [Biochemistry (Wash.)], (20010400) vol. 40, no. 13, pp. 3985-3995. ISSN: 0006-2960.
DOCUMENT TYPE: Journal
FILE SEGMENT: J
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Pilin is the major structural **protein** that forms type IV pili of various pathogenic bacteria, including Pseudomonas aeruginosa. Pilin is involved in attachment of the bacterium to host cells during infection, in the initiation of immune response, and serves as a receptor for a variety of bacteriophage. We have used super(15)N nuclear **magnetic** resonance relaxation measurements to **probe** the backbone dynamics of an N-terminally truncated monomeric pilin from P. aeruginosa strain K122-4. super(15)N-T sub(1), -T sub(2), and { super(1)H}- super(15)N nuclear Overhauser enhancement measurements were carried out at three **magnetic** field strengths. The measurements were interpreted using the Lipari-Szabo model-free analysis, which reveals the amplitude of **spatial** restriction for backbone N-NH bond vectors with respect to nano- to picosecond time-scale motions. Regions of well-defined secondary structure exhibited consistently low-amplitude **spatial** fluctuations, while the terminal and loop regions showed larger amplitude motions in the subnano- to picosecond time-scale. Interestingly, the C-terminal disulfide loop region that contains the receptor **binding** domain was found to be relatively rigid on the pico- to nanosecond time-scale but exhibited motion in the micro- to millisecond time-scale. It is notable that this disulfide loop displays a conserved antigenic epitope and mediates **binding** to the asialo-GM sub(1) cell surface receptor. The present study suggests that a rigid backbone scaffold mediates attachment to the host cell receptor, and also maintains the conformation of the conserved antigenic epitope for antibody recognition. In addition, slower millisecond time-scale motions are likely to be crucial for conferring a range of specificity for these interactions. Characterization of pilin dynamics will aid in developing a detailed understanding of infection, and will facilitate the design of more efficient anti-adhesin synthetic vaccines and therapeutics against pathogenic bacteria containing type IV pili.

L19 ANSWER 6 OF 20 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 2001:32039751 BIOTECHNO

TITLE: Membrane **binding** motif of the P-type cardiotoxin
AUTHOR: Dubovskii P.V.; Dementieva D.V.; Bocharov E.V.; Utkin Y.N.; Arseniev A.S.
CORPORATE SOURCE: A.S. Arseniev, Shemyakin and Ovchinnikov, Institute of Bioorganic Chemistry, Russian Academy of Sciences, 16/10 Miklukho-Maklaya str., V-437 Moscow, Russian Federation.
E-mail: aars@nmr.ru
SOURCE: Journal of Molecular Biology, (05 JAN 2001), 305/1 (137-149), 48 reference(s)
CODEN: JMOBAK ISSN: 0022-2836
DOCUMENT TYPE: Journal; Article
COUNTRY: United Kingdom
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2001:32039751 BIOTECHNO
AB Carditoxins (CTXs) from cobra snake venoms, the basic 60-62 residue all-beta sheet polypeptides, are known to **bind** to and impair the function of cell membranes. To assess the membrane induced conformation and orientation of CTXs, the interaction of the P-type cardiotoxin II from Naja oxiana snake venom (CTII) with perdeuterated dodecylphosphocholine (DPC) was studied using .sup.1H-NMR spectroscopy and diffusion measurements. Under conditions where the toxin formed a well-defined complex with DPC, the **spatial** structure of CTII with respect to the presence of tightly **bound** water molecules in loop II, was calculated using the torsion angle dynamics program DYANA. The structure was found to be similar, except for subtle changes in the tips of all three loops, to the previously described "major" form of CTII in aqueous solution illustrated by the "trans" configuration of the Val7-Pro8 **peptide** bond. No "minor" form with the "cis" configuration of the above bond was found in the micellebound state. The broadening of the CTII backbone proton signals by 5, 16-doxylstearate relaxation **probes**, together with modeling based on the **spatial** structure of CTII, indicated a periphery mode of **binding** of the toxin molecule to the micelle and revealed its micelle interacting domain. The latter includes a hydrophobic region of CTII within the extremities of loops I and III (residues 5-11, 46-50), the basement of loop II (residues 24-29,31-37) and the belt of polar residues encircling these loops (lysines 4,5,12,23,50, serines 11,46, histidine 31, arginine 36). It is suggested that this structural motif and the mode of **binding** can be realized during interaction of CTXs with lipid and biological membranes. .COPYRGT. 2001 Academic Press.

L19 ANSWER 7 OF 20 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 1999:29187488 BIOTECHNO
TITLE: Nuclear **magnetic** resonance study of the flavoprotein component of the Escherichia coli sulfite reductase
AUTHOR: Evrard A.; Zeghouf M.; Fontecave M.; Roby C.; Coves J.
CORPORATE SOURCE: J. Coves, Laboratoire de Chimie et Biochimie, Centres Redox Biologiques, Universite Joseph Fourier, 17 Avenue des Martyrs, 38054 Grenoble Cedex 9, France.
E-mail: coves@cbcrb.ceng.cea.fr
SOURCE: European Journal of Biochemistry, (15 APR 1999), 261/2 (430-437), 29 reference(s)
CODEN: EJBCAI ISSN: 0014-2956
DOCUMENT TYPE: Journal; Article
COUNTRY: United Kingdom
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 1999:29187488 BIOTECHNO
AB SiR-FP60, the monomeric form of the Escherichia coli sulfite reductase flavoprotein component (SiR-FP), has been analysed by .sup.3.sup.1P-NMR

spectroscopy. This **protein** was reported previously as a reliable simplified model for native SiR-FP ¢Zeghouf, M., Fontecave, M., Macherel, D., and Coves, J. (1998) Biochemistry 37, 6117-6123!. SiR-FP60 was examined in its native form, as a complex with NADP.sup.+ and after monoelectronic reduction either with NADPH or dithionite. In these latter cases, the stabilized FMN semiquinone radical offers a natural and internal paramagnetic **probe**. The paramagnetic effect of added manganese was also studied. In each case, the NMR parameters were extracted from digitalized data by a deconvolution procedure and compared with those obtained previously with cytochrome P450 reductase. Evolution of the NMR parameters and of calculated relaxation rate constants upon biochemical modifications of SiR-FP60 led us to propose that the reactive center is more compact than the one of cytochrome P450 reductase, with the redox components, FMN, FAD and NADPH, in a tighter **spatial** arrangement, close to the **protein** surface. This underlies some subtle differences between the two **proteins** for which a very similar overall structure is likely considering their common genetic origin and common operating cycle.

L19 ANSWER 8 OF 20 LIFESCI COPYRIGHT 2005 CSA on STN
ACCESSION NUMBER: 1999:6507 LIFESCI
TITLE: **Binding** of the nucleocapsid **protein** of type 1 human immunodeficiency virus to nucleic acids studied using phosphorescence and optically detected **magnetic** resonance
AUTHOR: Wu, J.Q.; Ozarowski, A.; Maki, A.H.; Urbaneja, M.A.; Henderson, L.E.; Casas-Finet, J.R.
CORPORATE SOURCE: Dep. Chem., Univ. California, Davis, CA 95616, USA
SOURCE: BIOCHEMISTRY (WASH.), (19971000) vol. 36, no. 41, pp. 12506-12518.
ISSN: 0006-2960.
DOCUMENT TYPE: Journal
FILE SEGMENT: V
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The **binding** of p7 nucleocapsid **protein** of type 1 human immunodeficiency virus (HIV-1) to various oligonucleotides and polynucleotides has been investigated by phosphorescence and optically detected **magnetic** resonance (ODMR) spectroscopy. The intrinsic spectroscopic **probe** used in these studies is the photoexcited triplet state of Trp37, which is associated with the C-terminal zinc finger of p7 and is its only tryptophan residue. Complex formation produces a red-shift of the phosphorescence 0,0-band (Delta E sub(0,0)) of Trp37 as well as a reduction of the zero field splitting (zfs) D parameter. Increases of - Delta E sub(0,0) (A < C < U < G < I) rank with increasing **binding** affinity to nucleic acid homooligomers (A similar to C < U < G similar to I). It is proposed that the **magnitude** of the shift reflects the extent of aromatic stacking interactions. We propose also that - Delta D increases not only with increased aromatic stacking but also with the extent of charge transfer (CT) character admixed into the triplet state. The quantity Delta D/ Delta E sub(0,0) correlates with the electron affinity of the bases (G < A < C < U approximately T), suggesting that this quantity reflects the extent of CT character admixed with the triplet state by the aromatic stacking interaction. Also affected by nucleic acid **binding** of p7 are the kinetic parameters of Trp37. We find a selective increase in the relative populating rate, and of the decay rate constant of the T sub(x) sublevel. In **binding** of p7 to either d(IT) sub(2) or d(IT) sub(4), two distinct sets of triplet states of Trp37 are resolved, suggesting the existence of specific nucleic acid **binding** modes of these heterooligomers.

L19 ANSWER 9 OF 20 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN

ACCESSION NUMBER: 1996:26342991 BIOTECHNO
TITLE: Anion **binding** to mitochondrial cytochromes c studied through electrochemistry. Effects of the neutralization of surface charges on the redox potential
AUTHOR: Battistuzzi G.; Borsari M.; Dallari D.; Lancellotti I.; Sola M.
CORPORATE SOURCE: Institute of Agricultural Chemistry, University of Bologna, Viale Berti Pichat 10,I-40127 Bologna, Italy.
SOURCE: European Journal of Biochemistry, (1996), 241/1 (208-214)
CODEN: EJBCAI ISSN: 0014-2956
DOCUMENT TYPE: Journal; Article
COUNTRY: Germany, Federal Republic of
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 1996:26342991 BIOTECHNO
AB The redox potential of horse and bovine heart cytochromes c determined through cyclic voltammetry is exploited to **probe** for anion-**protein** interactions, using a Debye-Huckel-based model. In parallel, **protein** charge neutralization resulting from specific anion **binding** allows monitoring for surface-charge/E° relationships. This approach shows that a number of anions, most of which are of biological relevance, namely Cl.sup.-, HPO.sub.4.sup.2.sup.-, HCO.sub.3.sup.-, NO.sub.3.sup.-, SO.sub.4.sup.2.sup.-, ClO.sub.4.sup.-, citrate.sup.3- and oxalate.sup.2.sup.-; **bind** specifically to the **protein** surface, often in a sequential manner as a result of the presence of multiple sites with different affinities. The **binding** stoichiometries of the various anions toward a given cytochrome are in general different. Chloride and phosphate appear to **bind** to a greater extent to both **proteins** as compared to the other anions. Differences in **binding** specificity toward the two cytochromes, although highly sequence-related, are observed for a few anions. The data are discussed comparatively in terms of electrostatic and geometric properties of the anions and by reference to the proposed location and amino acid composition of the anion **binding** sites, when available. Specific **binding** of this large set of anions bearing different charges allows the electrostatic effect on E° due to neutralization of net positive **protein** surface charge(s) to be monitored. .sup.1H NMR indeed indicates the absence of significant salt-induced structural perturbations, hence the above change in E° is predominantly electrostatic in origin. A systematic study of **protein** surface-charge/E° relationships using this approach is unprecedented. Values of 15-25 mV (extrapolated at zero ionic strength) are obtained for the decrease in E° due to neutralization of one positive surface charge, which are of the same order of **magnitude** as previous estimates obtained with either mutation or chemical modification of surface lysines. The effects of the anion-induced decrease of net positive charge on E° persist also at a relatively high ionic strength and add to the general effects related to the charge shielding of the **protein** as a whole due to the surrounding ionic atmosphere: hence the ionic strength dependence of the rate of electrontransfer between cytochromes c and redox partners could also involve salt-induced changes in the driving force.

L19 ANSWER 10 OF 20 BIOTECHNO
ACCESSION NUMBER: 1995:25317382 BIOTECHNO
TITLE: Imino proton exchange provides an .sup.1H-NMR footprint of **protein-DNA** interactions: General strategy and application to the SRY HMG box.sup.+
AUTHOR: Weiss M.A.; King C.-Y.
CORPORATE SOURCE: DBCMP, Harvard Medical School,Boston, MA 02115, United

States.
SOURCE: Journal of Biomolecular Structure and Dynamics, (1995), 13/2 (261-268)
CODEN: JBSDD6 ISSN: 0739-1102
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 1995:25317382 BIOTECHNO
AB A novel .sup.1H nuclear **magnetic** resonance (NMR) strategy for 'footprinting' specific **protein-DNA target** sites is demonstrated. Relative rates of site- specific imino-proton exchange in the free and **bound DNA** duplex are determined by use of laminar-shifted shaped pulses in NOESY spectra. 2D exchange crosspeaks between imino (ω.sub.2 dimension) and water (ω.sub.1 dimension) resonances in principle provide site-specific **probes** of **protein binding**. Chemical exchange is distinguished from nuclear Overhauser enhancements (NOEs) to **bound** water by use of ROESY spectroscopy. This strategy is illustrated in .sup.1H-NMR studies of the SRY high-mobility group (HMG) box, the Y-chromosome-encoded 'master switch' for testis determination in man, in a specific complex between the **protein** and a 15-basepair **DNA** site, imino- proton exchange was observed to be damped selectively within the six basepair subsite 5'-ATTGTT, previously identified by random **binding**-site selection as an optimal SRY **target** sequence. The extent of damping correlates with sites of **protein-DNA** contacts in the minor groove but not with the **magnitude** of .sup.1H-NMR complexation shifts. SRY **binding** has recently been shown to introduce significant distortions in **DNA** structure. The **DNA** is sharply bent and underwound; the minor groove is widened and major groove compressed. Our results demonstrate that despite such distortions base pairing is stably maintained. **Protein binding** in the **DNA** minor groove shields **DNA** imino protons from exchange with solvent.

L19 ANSWER 11 OF 20 LIFESCI COPYRIGHT 2005 CSA on STN
ACCESSION NUMBER: 97:5804 LIFESCI
TITLE: The development of single molecule environmental sensors
AUTHOR: Smith, C.L.; Kricka, L.; Krull, U.J.
CORPORATE SOURCE: Cent. for Advanced Biotechnol. and Dep. Biomed. Eng., Biol. and Pharmacol., Boston, MA Univ., 36 Cummington St., Boston, MA 02215, USA
SOURCE: GENET. ANAL. BIOMOL. ENGIN., (1995) vol. 12, no. 1, pp. 33-37.
ISSN: 1050-3862.
DOCUMENT TYPE: Journal
TREATMENT CODE: General Review
FILE SEGMENT: W2
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Leuwenhook first detected microbes by looking at water droplets in the microscope. Since then, the microscope has proven to be a powerful tool to identify specific organisms not only by their size and shape but, also, aided by simple differential staining methods. Microbiologists throughout the world are quite adept at identifying a wide variety of microorganisms this way. The universality of this method is probably partly due to the transportability of the microscope, the identifying information and its low maintenance cost. Along with direct observation, culture methods, which are more or less selective, allow for logarithmic amplification and, hence, enhanced detection of those organisms which can be grown. While culture methods in combination with various tests continue to be an important technique in the analysis of bacterial contamination, they are unsuitable for rapid assays, are difficult to use if a wide variety of

bacteria are in a sample, and may be impossible to use if the **target** organism is not known. It is estimated that less than 20% of the total number of different types of microorganisms have been identified using these traditional methods. It is quite clear that there is a need for rapid, simple and reliable detection methods of low numbers of or even single organisms (1.7 yoctomoles, 1.7 x 10 super(-23) moles), for instance food production and environmental and clinical monitoring applications. In many situations, the detection need is focused on well-characterized microorganisms that, for instance, cause disease or have been released for bioremediation. However, sensitive technology also promises to let us learn about heretofore unknown organisms important in particular ecosystems (e.g. the estimated 5000 different organisms believed to be present in sludge) that have not been grown in culture. The ability to detect microorganisms in the laboratory at low, even single cell or molecule amounts is theoretically possible. For instance, a number of biosensors which mimic the great amplification power of living systems have the potential to detect single organisms. However, the application of current laboratory methods to detecting organisms in the environment presents additional problems like increased background noise. The latter comprises several components (detector noise, reagent blank, non-specific **binding**), all of which limit achievable detection sensitivity and are somewhat method specific. Another key consideration is sample acquisition. For instance, a sample collected by washing food or soil will not necessarily provide bacteria because these microorganisms tend to tenaciously cling to such matrices. Thus, it is important to determine what amount of sample must be tested to provide a statistically significant result. There are a number of ways of dissecting the problem. For instance, it is clear that in some cases large volumes of liquids or solids must be tested. For liquids, one might imagine throwing a molecular hook attached to a **magnetic** particle into a sample to capture **targets** and then recapturing the hook with a magnet. The capture and detection methods can either be designed to use **probe** arrays (for molecular fingerprinting of single **targets**) or use **target** arrays (which will be analyzed in a parallel fashion). Such arrays can be scanned, with or without amplification, by a number of optical, electrical or thermal methods depending on the type of tag that is used (see below). Alternatively, flow methods using on line biosensors might be more appropriate for monitoring some liquids. Solids might be monitored using nanomolecular hooks that are subsequently captured. Alternatively, in situ detection methods may be important when dealing with solids in order to gather **spatial** information. (DBO)

L19 ANSWER 12 OF 20 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 1994:24366689 BIOTECHNO
TITLE: **Binding** of a new Ca.sup.2.sup.+ sensitizer, levosimendan, to recombinant human cardiac troponin C. A molecular modelling, fluorescence **probe**, and proton nuclear **magnetic** resonance study
AUTHOR: Pollesello P.; Ovaska M.; Kaivola J.; Tilgmann C.; Lundstrom K.; Kalkkinen N.; Ulmanen I.; Nissinen E.; Taskinen J.
CORPORATE SOURCE: Chemical Research Dept., Orion-Farmos, Orion Corp., P.O. Box 65,FIN-02101 Espoo, Finland.
SOURCE: Journal of Biological Chemistry, (1994), 269/46 (28584-28590)
CODEN: JBCHA3 ISSN: 0021-9258
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 1994:24366689 BIOTECHNO
AB The **binding** of a new calcium sensitizer, levosimendan, to human cardiac troponin C (cTnC) is described. Fluorescence studies done on dansylated recombinant human cTnC and a site-directed mutant showed that

levosimendan modulated the calcium-induced conformational change in cTnC, and revealed the role of Asp-88 in the **binding** of the drug to the NH.sub.2-terminal domain of cTnC. Furthermore, NMR studies performed on the NH.sub.2-terminal fragment of cTnC showed a **spatial** proximity between levosimendan and Met.sup.8.sup.1, Met.sup.8.sup.5, and Phe.sup.7.sup.7 in the drug-**protein** complex. These data were used to build an optimized model of the drug-**protein** complex, in which levosimendan **binds** cTnC at the hydrophobic pocket of the NH.sub.2-terminal domain. The role of the **binding** of levosimendan to cTnC in the pharmacological action of this drug in vivo is discussed.

L19 ANSWER 13 OF 20 LIFESCI COPYRIGHT 2005 CSA on STN
ACCESSION NUMBER: 95:25126 LIFESCI
TITLE: Phosphorescence and optically detected **magnetic** resonance investigation of the **binding** of the nucleocapsid **protein** of the human immunodeficiency virus type 1 and related **peptides** to **RNA**
AUTHOR: Lam, Wai-Chung; Maki, A.H.*; Casas-Finet, J.R.; Erickson, J.W.; Kane, B.P.; Sowder, R.C.,II; Henderson, L.E.
CORPORATE SOURCE: Dep. Chem., Univ. California, Davis, CA 95616, USA
SOURCE: BIOCHEMISTRY (WASH.), (1994) vol. 33, no. 35, pp. 10693-10700.
ISSN: 0006-2960.
DOCUMENT TYPE: Journal
FILE SEGMENT: N; V
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The **RNA** and **DNA** complexes of nucleocapsid **protein** p7.Zn (NCp7.Zn) of the human immunodeficiency virus type 1 (HIV-1) are studied by phosphorescence and optically detected **magnetic** resonance (ODMR). The single tryptophan, Trp37, which is located on the C-terminal zinc finger domain is used as an intrinsic **probe**. Reductions in the triplet state zero-field splitting (zfs) D parameter of Trp37 upon complex formation with poly(I) and poly(U) are observed. These results, in conjunction with the phosphorescence red-shifts and triplet state lifetime reductions that are observed, suggest the presence of aromatic stacking interactions between NCp7.Zn and the bases of the **RNA** polymers. An alteration of the intersystem crossing pattern upon complex formation, in addition to the above mentioned spectroscopic shifts, also is consistent with previously observed tryptophans that undergo stacking interactions with **DNA** bases. These conclusions support those from a recent ODMR study of NCp7.Zn **binding** to 5-mercurated polyuridylic acid [poly(5-HgU)] in which stacking interactions between the **RNA** and NCp7.Zn are inferred from the observation of an external heavy atom effect induced on Trp37. The extent of the spectroscopic effects observed varies with different **RNA** complexes; the phosphorescence red-shifts, for instance, correlate with the affinities of NCp7.Zn for various **RNA** bases as measured by fluorescence quenching experiments. The complexes of an 18mer synthetic second zinc finger **peptide** of NCp7 with **RNA** polymers gave results similar to NCp7.Zn, indicating that tryptophan in either the wild type **protein** or in the synthetic **peptide** experience similar environments. However, spectroscopic effects of smaller **magnitude** are observed in the synthetic second zinc finger **peptide** complexes, relative to those in the NCp7.Zn complexes, suggesting that the two zinc fingers in NCp7.Zn may act in concert to **bind** **RNA**. A synthetic carboxymethylated second zinc finger **peptide** in which a zinc finger structure cannot be formed also is studied. The triplet state properties observed for the uncomplexed synthetic carboxymethylated second zinc finger **peptide** are similar to those of the noncarboxymethylated synthetic second zinc finger **peptide**, suggesting that the tryptophans in

the two fingers have similar environments in the uncomplexed form. When either poly(I) or poly(U) is added to the synthetic carboxymethylated second zinc finger **peptide**, practically no spectroscopic effects are observed, indicating weak or no interaction between Trp37 and the **RNAs** under experimental conditions similar to those used for NCp7.Zn and the synthetic second zinc finger **peptide** **binding**.

L19 ANSWER 14 OF 20 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 1994:24150977 BIOTECHNO
TITLE: Role of the interdomain hinge of flavocytochrome b.sub.2 in intra- and inter- **protein** electron transfer
AUTHOR: Sharp R.E.; White P.; Chapman S.K.; Reid G.A.
CORPORATE SOURCE: Department of Chemistry, Institute of Cell/Molecular Biology, University of Edinburgh, Mayfield Road,Edinburgh EH9 3JR, United Kingdom.
SOURCE: Biochemistry, (1994), 33/17 (5115-5120)
CODEN: BICHAW ISSN: 0006-2960
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 1994:24150977 BIOTECHNO
AB The two distinct domains of flavocytochrome b.sub.2 (L-lactate:cytochrome c oxidoreductase, EC 1.1.2.3) are connected by a hinge **peptide**. Kinetics experiments ¢White, P., Manson, F. D. C., Brunt, C. E., Chapman, S. K., and Reid, GA. (1993) Biochem. J. 291, 89-94! have illustrated the importance for efficient interdomain electron transfer of maintaining the structural integrity of the hinge. To **probe** the role of the hinge in a more subtle manner, we have constructed a mutant enzyme, HΔ3, which has a three amino acid deletion in the hinge region. Intra- and inter-**protein** electron transfer within HΔ3 flavocytochrome b.sub.2 and the HΔ3:cytochrome c redox complex was investigated by steady-state and stopped-flow kinetics analysis. The HΔ3 mutant enzyme remains a good L-lactate dehydrogenase, as is evident from steady-state experiments with ferricyanide as electron acceptor (40% less active than wild-type enzyme) and stopped-flow experiments monitoring flavin reduction (15% less active than wild type enzyme). The global effect of the deletion is to lower the enzyme's effectiveness as a cytochrome c reductase. This property of the HΔ3 enzyme is manifested at two electron-transfer steps on the catalytic cycle of flavocytochrome b.sub.2. First, the rate of heme reduction has fallen 5-fold in HΔ3 compared with the wild-type enzyme (from 445 to 91 s.sup.-.sup.1), due to poor interdomain electron transfer from flavin to heme. Second, the rate of cyclochrome c reduction in the steady-state has fallen 5-fold (from 207 to 39 s.sup.-.sup.1), indicating that b.sub.2 heme to cytochrome c electron transfer has also been disrupted. These data, along with the measured kinetic isotope effects, indicate that cytochrome c reduction has become the rate-limiting step in the catalytic cycle for the HΔ3 enzyme. Further evidence for the importance of the hinge in inter-**protein** electron transfer is obtained from second-order rate constants for cytochrome c reduction by prereduced flavocytochrome b.sub.2: the rate constant for HΔ3 is an order of **magnitude** less than the corresponding value for the wild-type enzyme, with values of 4 x 10.sup.6 and 4.7 x 10.sup.7 M.sup.-.sup.1 s.sup.-.sup.1, respectively. From our data, we conclude that the hinge plays an important role in facilitating both intra- and inter-**protein** electron transfer.

L19 ANSWER 15 OF 20 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
DUPLICATE
ACCESSION NUMBER: 1993:23234762 BIOTECHNO
TITLE: Evidence for stacking interactions between

5-mercurated polyuridylic acid and HIV-1 p7 nucleocapsid **protein** obtained by phosphorescence and optically detected **magnetic** resonance (ODMR)

AUTHOR: Lam W.-C.; Maki A.H.; Casas-Finet J.R.; Erickson J.W.; Sowder II R.C.; Henderson L.E.

CORPORATE SOURCE: Department of Chemistry, University of California,Davis, CA 95616, United States.

SOURCE: FEBS Letters, (1993), 328/1-2 (45-48)
CODEN: FEBLAL ISSN: 0014-5793

DOCUMENT TYPE: Journal; Article

COUNTRY: Netherlands

LANGUAGE: English

SUMMARY LANGUAGE: English

AN 1993:23234762 BIOTECHNO

AB The photoexcited triplet state of Trp-37 in the C-terminal zinc finger of the HIV-1 p7 nucleocapsid **protein** was used as a **probe** of p7 interactions with the heavy atom-derivatized **RNA** homopolymer, poly-5-mercuriuridylic acid (5-HgU). **Binding** of p7 to 5-HgU (Hg blocked with 2-mercaptoethanol) produces an external heavy atom effect (HAE) on Trp-37 characterized by fluorescence quenching, reduction of the phosphorescence lifetime by three orders of **magnitude**, and the appearance of the D + E phosphorescence-detected ODMR signal, absent in unperturbed Trp, but induced by a HAE. The details of the HAE are consistent with out-of-plane van der Waals contact of Hg with the indole chromophore of Trp-37. Steric requirements suggest further that the Trp-**RNA** contact occurs via an aromatic stacking interaction.

L19 ANSWER 16 OF 20 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN

ACCESSION NUMBER: 1992:22340900 BIOTECHNO

TITLE: Thermal motions of surface α-helices in the D-galactose chemosensory receptor. Detection by disulfide trapping

AUTHOR: Careaga C.L.; Falke J.J.

CORPORATE SOURCE: Dept of Chemistry and Biochemistry, University of Colorado,Boulder, CO 80309-0215, United States.

SOURCE: Journal of Molecular Biology, (1992), 226/4 (1219-1235)
CODEN: JMOBAK ISSN: 0022-2836

DOCUMENT TYPE: Journal; Article

COUNTRY: United Kingdom

LANGUAGE: English

SUMMARY LANGUAGE: English

AN 1992:22340900 BIOTECHNO

AB The D-galactose chemosensory receptor of Escherichia coli is a 32 kDa globular **protein** possessing two distinct structural domains, each organized in an α/β folding motif. Helices I and X lie at adjacent approximately parallel positions on the surface of the N-terminal domain, near the hinge region. In order to analyze the relative thermal motions of these two helices, the present study utilizes a generalizable disulfide trapping approach: first, site-directed mutagenesis is used to place a pair of cystein residues at locations of interest on the **protein** surface, then disulfide bond formation id used to trap intramolecular cysteine-cysteine collisions resulting from thermal motions. Specifically, four engineered di-cysteine receptors have been constructed, each possessing one cysteine at position 26 on helix I, and a second cysteine at varying positions on helix X. A fifth control receptor possesses one cysteine at position 26, and a second on the opposite surface of the molecule. These surface cysteine substitutions have little or no effect on the measurable receptor parameters as judged by ligand **binding** equilibria and kinetics, **protein** stability, and .sup.1.sup.9F nuclear **magnetic** resonance, indicating that the engineered receptors are useful

probes of native backbone dynamics. **Spatial** and kinetic features of backbone motions have been investigated by measuring intramolecular disulfide formation rates for cysteine pairs in the fully liganded receptor. The resulting rates decrease monotonically with increasing distance between cysteines in the crystal structure, while no disulfide formation is observed for the control pair unless the molecule is unfolded. The minimum translational amplitudes of the observed backbone motions range from 4.5 to 15.2 Å, and the minimum rotational amplitudes area as large as 35°. For each motion the rate of intramolecular sulfhydryl-sulfhydryl collision has been estimated from the measured rate of disulfide formation: the 4.5 and 15.2 Å translations yield .sim.10.sup.4 and .sim.10 collisions s.sup.-.sup.1 molecule.sup.-.sup.1, respectively. These collision rates, which are faster than ligand dissociation, likely underestimate the actual motional frequencies since only an undetermined fraction of the total motions yield collisions. The simplest plausible trajectory capable of producing such collisions is a rate-limiting translation of one or both helices along their long axes, coupled with minor helix rotations. When sugar is removed from the receptor, a substantial increase in backbone dynamics is observed, indicating the presence of new long-range backbone trajectories. Overall, the results suggest that internal motions in **proteins** may have larger amplitudes than previously observed.

L19 ANSWER 17 OF 20 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 1992:22093079 BIOTECHNO
TITLE: Location of potential **binding** sites on deoxy hemoglobin for the design of antigelling agents
AUTHOR: Manavalan P.; Prabhakaran M.; Johnson M.E.
CORPORATE SOURCE: Dept. of Medicinal Chemistry, Univ. of Illinois at Chicago, P.O. Box 6998,Chicago, IL 60680, United States.
SOURCE: Journal of Molecular Biology, (1992), 223/3 (791-800)
CODEN: JMOBAK ISSN: 0022-2836
DOCUMENT TYPE: Journal; Article
COUNTRY: United Kingdom
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 1992:22093079 BIOTECHNO
AB The **binding** sites of indole-based gelation inhibitors with sickle cell hemoglobin were investigated by two parallel theoretical approaches. A geometric approach originated by Kuntz and co-workers uses a **spatial** buildup scheme to locate potential **binding** regions, while a hybrid grid/geometric search method searches for specific indole ring **binding** pockets over the hemoglobin surface. The **binding** sites derived from these calculations were tested for their ability to accommodate indole rings by means of accessibility calculations with **probes** of various radii. These sites were further scanned for van der Waals' overlap and electrostatic interactions. A full 5BrTrp residue was built in each indole ring **binding** site, and its conformational energy of association with sickle hemoglobin was calculated at that site. Our theoretical results predict a total of 14 potential **binding** regions, including all of the sites observed from X-ray crystallography, and sites that are consistent with solution nuclear **magnetic** resonance studies.

L19 ANSWER 18 OF 20 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 1992:22344422 BIOTECHNO
TITLE: Interaction of calmodulin with phospholamban and caldesmon: Comparative studies by .sup.1H-NMR spectroscopy
AUTHOR: Gao Y.; Levine B.A.; Mornet D.; Slatter D.A.; Strasburg G.M.
CORPORATE SOURCE: School of Biochemistry, University of Birmingham,Birmingham B15 2TT, United Kingdom.

SOURCE: Biochimica et Biophysica Acta - Protein Structure and Molecular Enzymology, (1992), 1160/1 (22-34)
CODEN: BBAEDZ ISSN: 0167-4838
DOCUMENT TYPE: Journal; Conference Article
COUNTRY: Netherlands
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 1992:22344422 BIOTECHNO
AB In order to identify comparative aspects of the interaction of calmodulin with its **target proteins**, proton **magnetic** -resonance studies of complex formation between calmodulin and defined segments of phospholamban and caldesmon have been undertaken. Residues 3-15 in the cytoplasmic region of phospholamban, an integral membrane **protein** of cardiac sarcoplasmic reticulum believed to regulate the calcium pumping ATPase, are shown to contribute to interaction with calmodulin. Using wheat germ calmodulin specifically modified with a spin-label to provide the spectral means for **spatial** localisation, these residues of phospholamban were correlated with **binding** in the vicinity of the **probe** attached to Cys-27 in the N-terminal domain of calmodulin. This interaction, relevant to the mechanism of calmodulin-dependent phosphorylation of phospholamban that relieves its inhibitory influence on the calcium pump, provides a useful model system for comparative study of the properties of calmodulin-**binding** domains. We contrast here a calmodulin-**binding** segment in the C-terminal region of caldesmon localised by .sup.1H-NMR study of the interface(s) between the two **proteins**. These observations are discussed in the context of other calmodulin-**binding** sequences.

L19 ANSWER 19 OF 20 LIFESCI COPYRIGHT 2005 CSA on STN
ACCESSION NUMBER: 82:13035 LIFESCI
TITLE: Direct Observations of the super(43)Ca NMR Signals From Ca super(2+) Ions **Bound** to **Proteins**.
AUTHOR: Andersson, T.; Drakenberg, T.; Forsen, S.; Thulin, E.; Swaerd, M.
CORPORATE SOURCE: Dep. Physical Chem. 1, Chem. Cent., Univ. Lund, S-220 07, Sweden
SOURCE: J. AM. CHEM. SOC., (1982) vol. 104, no. 2, pp. 576-580.
DOCUMENT TYPE: Journal
FILE SEGMENT: T
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The super(43)Ca NMR signals from Ca super(2+) ions **bound** to the Ca super(2+) **binding proteins** parvalbumin, troponin C, and calmodulin have been observed. The observation was made possible through the combined use of isotopically enriched super(43)Ca super(2+), FT techniques, high **magnetic** fields, and a solenoid type of **probe** design. Measurements of the apparent longitudinal relaxation rate, R sub(1), and the transverse relaxation rate, R sub(2), provide values of both the quadrupole coupling constant and the correlation time. The **magnitude** of the calculated correlation times is in good agreement with the rotational correlation time for the entire **protein** molecules, indicating the Ca super(2+)-**binding** sites to have a comparatively rigid structure.

L19 ANSWER 20 OF 20 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 1981:11157227 BIOTECHNO
TITLE: A .sup.1H nuclear relaxation study of the Mn.sup.2.sup.+. Bleomycin complex. Proximity of the metal to the **DNA-binding** site
AUTHOR: Sheridan R.P.; Gupta R.K.
CORPORATE SOURCE: Inst. Cancer Res., Fox Chase Cancer Cent., Philadelphia, Pa. 19111, United States.
SOURCE: Journal of Biological Chemistry, (1981), 256/3

(1242-1247)
CODEN: JBCHA3
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
AN 1981:11157227 BIOTECHNO
AB The antineoplastic action of bleomycin is thought to involve the aerobic degradation of **DNA** by the Fe.sup.2.sup.+ . bleomycin complex. Different parts of the bleomycin molecule have been implicated in metal **binding** and **DNA binding**. To **probe** the structure of a metal-containing bleomycin, the authors studied the effects of the high spin Mn.sup.2.sup.+ ion in the Mn.sup.2.sup.+ .midldot. bleomycin complex on the longitudinal nuclear relaxation rates of various protons in the molecule. Complexation of Mn.sup.2.sup.+ to bleomycin was also studied by EPR, and a Scatchard plot of the EPR data revealed a single tight divalent cation-**binding** site per molecule. From the **magnitudes** of the paramagnetic effects of Mn.sup.2.sup.+ on the nuclear relaxation rates of several assigned resonances, the authors calculate the relative distances of the corresponding protons from the metal. Using a pyrimidine methyl to metal distance of 6.5 Å, consistent with the metal coordination of this aromatic group of bleomycin established on the basis of other studies, the authors find from their data that the bithiazole and COOH-terminal portions of the molecule are located spatially very close to the metal. These groups have previously been implicated in **DNA binding**. The authors metal to bithiazole proton distances (.sim. 5.4Å) are consistent with bithiazole as a metal ligand, although possible involvement of interactions other than direct coordination in maintaining close proximity cannot be excluded. The authors distance data also argue against the imidazole ring of β-hydroxyhistidine as a ligand. The short distance between the metal- and **DNA-binding** sites indicated by the authors studies would help ensure that the reactive reduced oxygen radicals produced at the metal site during Fe.sup.2.sup.+ oxidation in the aerobic Fe.sup.2.sup.+ .midldot. bleomycin complex reach the substrate **DNA** before the destruction of these radicals can occur in other ways.

=> (swing or spatial or remant or coercive or magnitude) and (magnetic field) and (target or DNA or RNA or protein or peptide) and (binding or bind or bound)
L20 0 FILE AGRICOLA
L21 4 FILE BIOTECHNO
L22 0 FILE CONFSCI
L23 0 FILE HEALSAFE
L24 0 FILE IMSDRUGCONF
L25 5 FILE LIFESCI
L26 0 FILE MEDICONF
L27 3 FILE PASCAL

TOTAL FOR ALL FILES
L28 12 (SWING OR SPATIAL OR REMANT OR COERCIVE OR MAGNITUDE) AND (MAGNETIC FIELD) AND (TARGET OR DNA OR RNA OR PROTEIN OR PEPTIDE) AND (BINDING OR BIND OR BOUND)

=> dup rem
ENTER L# LIST OR (END):l28
DUPLICATE IS NOT AVAILABLE IN 'IMSDRUGCONF, MEDICONF'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L28
L29 12 DUP REM L28 (0 DUPLICATES REMOVED)

=> d l29 ibib abs total

L29 ANSWER 1 OF 12 PASCAL

on STN
ACCESSION NUMBER: 2004-0415820 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2004 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): New OH masers at 13 441 MHz
AUTHOR: CASWELL J. L.
CORPORATE SOURCE: Australia Telescope National Facility, CSIRO, PO Box 76, Epping, NSW 2121, Australia
SOURCE: Monthly Notices of the Royal Astronomical Society, (2004), 352(1), 101-111, 18 refs.
ISSN: 0035-8711 CODEN: MNRAA4
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United Kingdom
LANGUAGE: English
AVAILABILITY: INIST-2067, 354000120101050090
AN 2004-0415820 PASCAL
CP Copyright .COPYRGT. 2004 INIST-CNRS. All rights reserved.
AB The Parkes radio telescope has been used to study maser emission from the 13441-MHz transition of highly excited OH. The **targets** were 56 catalogued sites of 6035-MHz maser emission. Eight 13 441-MHz maser sites were detected, six of them new and two that had previously been reported. This more than doubles the number now known to 11. At every 13 441-MHz maser site, spectral features occur as right- and left-hand circularly polarized matched pairs, with small, but mostly significant, frequency separation. This is attributed to the Zeeman effect in **magnetic fields** of a few mG. Some of the 13 441-MHz maser sites show features at several different velocities. All of the 13441-MHz maser features have 6035-MHz counterparts that closely correspond in velocity. At three sites, features of 13 441-MHz emission rival the intensities of their 6035-MHz counterparts; at the other sites, features are weaker than at 6035 MHz by factors of between 3 and 50. Upper limits at some sites searched can be set more than 2 orders of **magnitude** weaker than 6035-MHz emission. The detection statistics provide unique opportunities to test recent advances in maser modelling. A search for the 13 434-MHz transition towards the same 56 **targets** yielded no detections.

L29 ANSWER 2 OF 12 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 2003:36020134 BIOTECHNO
TITLE: NMR detection of multiple transitions to low-populated states in azurin
AUTHOR: Korzhnev D.M.; Goran Karlsson B.; Orekhov V.Yu.; Billeter M.
CORPORATE SOURCE: M. Billeter, Biochemistry and Biophysics, Goteborg University, Box 462, 40530 Goteborg, Sweden.
E-mail: martin.billeter@bcbp.gu.se
SOURCE: Protein Science, (01 JAN 2003), 12/1 (56-65), 47 reference(s)
CODEN: PRCIEI ISSN: 0961-8368
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2003:36020134 BIOTECHNO
AB Transitions to conformational states with very low populations were detected for the reduced blue copper **protein** azurin from Pseudomonas aeruginosa by applying constant relaxation time CPMG measurements to the backbone .sup.1.sup.5N nuclei at three **magnetic fields** (11.7, 14.1, and 18.8 T) and three temperatures (25.7, 35.4, and 44.8°C). Two exchange processes with different rate constants could be discriminated despite populations of the excited states below 1% and **spatial** neighborhood of the two processes. The group of .sup.1.sup.5N nuclei involved in the faster process exhibits at 44.8°C a forward rate constant of 11.7±2.4

s.sup.-.sup.1 and a population of the exited state of 0.39±0.07%. They surround the aromatic ring of histidine 35 whose protonation state is coupled to the flipping of a neighboring **peptide** plane. For the slower process, the forward rate constant and population of the exited state at 44.8°C are 4.1±0.1 s.sup.-.sup.1 and 0.45±0.02%, respectively. The residues involved cluster nearby the copper ion, which is separated from the protonation site of histidine 35 by about 8 Å, indicating conformational rearrangements involving the copper coordinating loops. The dependence of the equilibrium constant on the temperature is consistent with an enthalpy-dominated transition around the copper, but an entropy-controlled transition near histidine 35. The detection by nuclear magnetic resonance of millisecond to second conformational transitions near the copper ion suggests a low energy-cost rearrangement of the copper-**binding** site that may be necessary for efficient electron transfer.

L29 ANSWER 3 OF 12 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 2002-0497055 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2002 American Institute of Physics. All rights reserved.
TITLE (IN ENGLISH): Magnetic gradiometer based on a high-transition temperature superconducting quantum interference device for improved sensitivity of a biosensor
AUTHOR: LEE SeungKyun; MYERS W. R.; GROSSMAN H. L.; CHO H.-M.; CHEMLA Y. R.; CLARKE John
CORPORATE SOURCE: Department of Physics, University of California, Berkeley, California 94720; Materials Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, California 94720
SOURCE: Applied physics letters, (2002-10-14), 81(16), 3094-3096
ISSN: 0003-6951 CODEN: APPLAB
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-10020
AN 2002-0497055 PASCAL
CP Copyright .COPYRGT. 2002 American Institute of Physics. All rights reserved.
AB We describe a gradiometer based on a high-transition temperature superconducting quantum interference device (SQUID) that improves the sensitivity of a SQUID-based biosensor. The first-derivative gradiometer, fabricated from a single layer of YBa.sub.2Cu.sub.3O.sub.7.sub.-.sub.x, has a baseline of 480 μm and a balance against uniform fields of 1 part in 150. Used in our SQUID microscope, it reduces the response to parasitic **magnetic fields** generated by the measurement process to the level of the SQUID noise. The gradiometer-based microscope is two orders of **magnitude** more sensitive to superparamagnetic nanoparticles **bound** to biological **targets** than our earlier magnetometer-based microscope. .COPYRGT. 2002 American Institute of Physics.

L29 ANSWER 4 OF 12 LIFESCI COPYRIGHT 2005 CSA on STN

ACCESSION NUMBER: 2001:98980 LIFESCI
TITLE: Backbone Dynamics of Receptor **Binding** and Antigenic Regions of a Pseudomonas aeruginosa Pilin Monomer
AUTHOR: Suh, Jeong-Yong; Spyracopoulos, L.; Keizer, D.W.; Irvin, R.T.; Sykes, B.D.
CORPORATE SOURCE: PENCE, 713 Heritage Medical Research Center, Edmonton, Alberta, T6G 2S2, Canada; E-mail: brian.sykes@ualberta.ca
SOURCE: Biochemistry (Washington) [Biochemistry (Wash.)], (20010400) vol. 40, no. 13, pp. 3985-3995.

ISSN: 0006-2960.
DOCUMENT TYPE: Journal
FILE SEGMENT: J
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Pilin is the major structural **protein** that forms type IV pili of various pathogenic bacteria, including Pseudomonas aeruginosa. Pilin is involved in attachment of the bacterium to host cells during infection, in the initiation of immune response, and serves as a receptor for a variety of bacteriophage. We have used super(15)N nuclear magnetic resonance relaxation measurements to probe the backbone dynamics of an N-terminally truncated monomeric pilin from P. aeruginosa strain K122-4. super(15)N-T sub(1), -T sub(2), and { super(1)H}- super(15)N nuclear Overhauser enhancement measurements were carried out at three **magnetic field** strengths. The measurements were interpreted using the Lipari-Szabo model-free analysis, which reveals the amplitude of **spatial** restriction for backbone N-NH bond vectors with respect to nano- to picosecond time-scale motions. Regions of well-defined secondary structure exhibited consistently low-amplitude **spatial** fluctuations, while the terminal and loop regions showed larger amplitude motions in the subnano- to picosecond time-scale. Interestingly, the C-terminal disulfide loop region that contains the receptor **binding** domain was found to be relatively rigid on the pico- to nanosecond time-scale but exhibited motion in the micro- to millisecond time-scale. It is notable that this disulfide loop displays a conserved antigenic epitope and mediates **binding** to the asialo-GM sub(1) cell surface receptor. The present study suggests that a rigid backbone scaffold mediates attachment to the host cell receptor, and also maintains the conformation of the conserved antigenic epitope for antibody recognition. In addition, slower millisecond time-scale motions are likely to be crucial for conferring a range of specificity for these interactions. Characterization of pilin dynamics will aid in developing a detailed understanding of infection, and will facilitate the design of more efficient anti-adhesin synthetic vaccines and therapeutics against pathogenic bacteria containing type IV pili.

L29 ANSWER 5 OF 12 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 2001-0270306 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2001 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): Integrin-mediated mechanotransduction in vascular smooth muscle cells : Frequency and force response characteristics
AUTHOR: GOLDSCHMIDT Marc E.; MCLEOD Kenneth J.; TAYLOR W. Robert
CORPORATE SOURCE: Cardiology Division, Department of Medicine, Atlanta VA Medical Center and Emory University School of Medicine, Atlanta, Ga, United States; Bioelectromagnetics Research Laboratory, Departments of Orthopaedics and Biomedical Engineering, State University of New York, Stony Brook, NY, United States
SOURCE: Circulation research, (2001), 88(7), 674-680, 32 refs. ISSN: 0009-7330 CODEN: CIRUAL
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-7216, 354000098211590070
AN 2001-0270306 PASCAL
CP Copyright .COPYRGT. 2001 INIST-CNRS. All rights reserved.
AB Blood vessels are continuously exposed to mechanical forces that lead to adaptive remodeling and atherosclerosis. Although there have been many studies characterizing the responses of vascular cells to mechanical

stimuli, the precise mechanical characteristics of the forces applied to cells to elicit these responses are not clear. We designed a magnetic exposure system capable of producing a defined normal force on ferromagnetic beads that are specifically **bound** to cultured cells coated with extracellular matrix **proteins** or integrin-specific antibodies. Rat aortic smooth muscle cells were incubated with engineered fibronectin-coated ferromagnetic beads and then exposed to a **magnetic field**. With activation of extracellular signal-regulated mitogen-activated **protein** kinase 1/2 (ERK 1/2.sup.M.sup.A.sup.P.sup.K) used as a prototypical marker for cell responsiveness to mechanical forces, Western blot analysis demonstrated an increase in phosphorylated ERK 1/2.sup.M.sup.A.sup.P.sup.K expression reaching a maximal response of a 3.5-fold increase at a total force of 2.5 pN per cell. The peak response occurred after 5 minutes of exposure and slowly decreased to baseline after 30 minutes. A cyclic, rather than static, force was required for this activation, and the frequency-response curve increased 2-fold between 0.5 and 2.0 Hz. Vitronectin- and β.sub.3 antibody-coated beads showed a response nearly identical to those coated with engineered fibronectin, whereas forces applied to beads coated with α.sub.2 and β.sub.1 antibodies did not significantly activate ERK 1/2.sup.M.sup.A.sup.P.sup.K. Mechanical activation of the ERK 1/2.sup.M.sup.A.sup.P.sup.K system in rat aortic smooth muscle cells occurs through specific integrin receptors and requires a cyclic force with a **magnitude** estimated to be in the piconewton range.

L29 ANSWER 6 OF 12 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 2000:32006235 BIOTECHNO
TITLE: Implementation of force differentiation in the immunoassay
AUTHOR: Lee G.U.; Metzger S.; Natesan M.; Yanavich C.; Dufrene Y.F.
CORPORATE SOURCE: G.U. Lee, Chemistry Division, Naval Research Laboratory, Washington, DC 20375-5342, United States. E-mail: gl@atom.ecn.purdue.edu
SOURCE: Analytical Biochemistry, (15 DEC 2000), 287/2 (261-271), 43 reference(s)
CODEN: ANBCA2 ISSN: 0003-2697
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2000:32006235 BIOTECHNO
AB A technique has been developed to apply force to the antibody-antigen complex in a solid-phase immunoassay. Force was applied to the immunochemical complex by labeling the secondary antibody with a magnetically susceptible, micrometer-size particle and placing the assay chamber in a **magnetic field** of defined **magnitude** and orientation. The force was strong enough to displace weakly **bound** particles but was not strong enough to rupture the immunochemical complex. The number of particles **bound** to the surface after applying the differentiation force was related to the analyte concentration, thus an optical detection scheme was developed for counting the number of particles on the surface. The sensitivity of the force differentiation assay was demonstrated to be one to two orders of **magnitude** higher than conventional solid-phase immunoassay techniques for model **protein**, virus, and bacterial analytes, with 99% specificity. The enhanced sensitivity of this assay appears to result from lowering the assay background through the identification of weakly adhesive, nonspecific interactions. (C) 2000 Academic Press.

L29 ANSWER 7 OF 12 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 1999:29518431 BIOTECHNO
TITLE: NMR approaches for monitoring domain orientations in

calcium-**binding proteins** in solution using partial replacement of Ca.sup.2.sup.+ by Tb.sup.3.sup.+

AUTHOR: Biekofsky R.R.; Muskett F.W.; Schmidt J.M.; Martin S.R.; Browne J.P.; Bayley P.M.; Feeney J.

CORPORATE SOURCE: J. Feeney, Molecular Structure Division, National Institute for Med. Research, The Ridgeway, Mill Hill, London NW7 1AA, United Kingdom.
E-mail: jfeeney@nimr.mrc.ac.uk

SOURCE: FEBS Letters, (1999), 460/3 (519-526), 40 reference(s)
CODEN: FEBLAL ISSN: 0014-5793

PUBLISHER ITEM IDENT.: S0014579399014106

DOCUMENT TYPE: Journal; Article

COUNTRY: Netherlands

LANGUAGE: English

SUMMARY LANGUAGE: English

AN 1999:29518431 BIOTECHNO

AB This work shows that the partial replacement of diamagnetic Ca.sup.2.sup.+ by paramagnetic Tb.sup.3.sup.+ in Ca.sup.2.sup.+/calmodulin systems in solution allows the measurement of interdomain NMR pseudocontact shifts and leads to magnetic alignment of the molecule such that significant residual dipolar couplings can be measured. Both these parameters can be used to provide structural information. Species in which Tb.sup.3.sup.+ ions are **bound** to only one domain of calmodulin (the N-domain) and Ca.sup.2.sup.+ ions to the other (the C-domain) provide convenient systems for measuring these parameters. The nuclei in the C-domain experience the local **magnetic field** induced by the paramagnetic Tb.sup.3.sup.+ ions **bound** to the other domain at distances of over 40 A from the Tb.sup.3.sup.+ ion, shifting the resonances for these nuclei. In addition, the Tb.sup.3.sup.+ ions **bound** to the N-domain of calmodulin greatly enhance the magnetic susceptibility anisotropy of the molecule so that a certain degree of alignment is produced due to interaction with the external **magnetic field**. In this way, dipolar couplings between nuclear spins are not averaged to zero due to solution molecular tumbling and yield dipolar coupling contributions to, for example, the one-bond .sup.1.sup.5N-.sup.1H splittings of up to 17 Hz in **magnitude**. The degree of alignment of the C-domain will also depend on the degree of orientational freedom of this domain with respect to the N-domain containing the Tb.sup.3.sup.+ ions. Pseudocontact shifts for NH groups and .sup.1H-.sup.1.sup.5N residual dipolar couplings for the directly bonded atoms have been measured for calmodulin itself, where the domains have orientational freedom, and for the complex of calmodulin with a **target peptide** from skeletal muscle myosin light chain kinase, where the domains have fixed orientations with respect to each other. The simultaneous measurements of these parameters for systems with domains in fixed orientations show great potential for the determination of the relative orientation of the domains.

L29 ANSWER 8 OF 12 LIFESCI COPYRIGHT 2005 CSA on STN

ACCESSION NUMBER: 97:1720 LIFESCI

TITLE: Bioeffects of weak combined, constant and variable **magnetic fields**

AUTHOR: Lednev, V.V.

CORPORATE SOURCE: Inst. Theoretical and Exptl. Biophys., Russian Acad. Sci., Pushchino (Moscow Region), Russia

SOURCE: BIOPHYSICS, (1996) vol. 41, no. 1, pp. 241-252.
ISSN: 0006-3509.

DOCUMENT TYPE: Journal

FILE SEGMENT: T

LANGUAGE: English

SUMMARY LANGUAGE: English

AB A model of the interaction of weak **magnetic fields**

with biosystems previously examined by the author for the case of pulse excitation of oscillators (ions **bound** in Ca super(2+)-dependent enzymes or **protein**-enzyme complexes) is extended to the case, more realistic for biosystems, of continuous excitation of the oscillators. Expressions are obtained for the degree of **spatial** polarization of the **swings** of the oscillators in combined, constant and variable fields. It is postulated that the size of the bioeffect induced in the biosystem by the **magnetic field** is proportional to the degree of polarization of the vibration of the ion. It is shown that the available experimental evidence accords with the predictions of theory.

L29 ANSWER 9 OF 12 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 1995:25193449 BIOTECHNO
TITLE: Rotational dynamics of calcium-free calmodulin studied by .sup.1.sup.5N-NMR relaxation measurements
AUTHOR: Tjandra N.; Kuboniwa H.; Ren H.; Bax A.
CORPORATE SOURCE: National Institutes of Health, Building 5,Bethesda, MD 20892-0520, United States.
SOURCE: European Journal of Biochemistry, (1995), 230/3 (1014-1024)
CODEN: EJBCAI ISSN: 0014-2956
DOCUMENT TYPE: Journal; Article
COUNTRY: Germany, Federal Republic of
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 1995:25193449 BIOTECHNO
AB The backbone motions of calcium-free Xenopus calmodulin have been characterized by measurements of the .sup.1.sup.5N longitudinal relaxation times (T.sub.1) at 51 and 61 MHz, and by conducting transverse relaxation (T.sub.2), spin- locked transverse relaxation (T(1ρ), and .sup.1.sup.5N-{.sup.1H} heteronuclear NOE measurements at 61 MHz .sup.1.sup.5N frequency. Although backbone amide hydrogen exchange experiments indicate that the N-terminal domain is more stable than calmodulin's C-terminal half, slowly exchanging backbone amide protons are found in all eight α-helices and in three of the four short β-strands. This confirms that the calcium-free form consists of stable secondary structure and does not adopt a 'molten globule' type of structure. However, the C- terminal domain of calmodulin is subject to conformational exchange on a time scale of about 350 μs, which affects many of the C-terminal domain residues. This results in significant shortening of the .sup.1.sup.5N T.sub.2 values relative to T(1ρ), whereas the T(1ρ) and T.sub.2. values are of **similar** magnitude in the N- terminal half of **the** protein. A model in which the motion of **the** protein is assumed to be isotropic suggests a rotational correlation time for **the** protein of about 8 ns but quantitatively does not agree with **the** **magnetic** field dependence of the T.sub.1 values and does not explain the different T.sub.2 values found for different α-helices in the N-terminal domain. These latter parameters are compatible with a flexible dumbbell model in which each of calmodulin's two domains freely diffuse in a cone with a semi-angle of about 30° and a time constant of about 3 ns. whereas the overall rotation of **the** protein occurs on a much slower time scale of about 12 ns. The difference in the transverse relaxation rates observed between the amides in helices C and D suggests that the change in interhelical angle upon **calcium** binding is less than predicted by Herzberg et al. Strynadka and James ¢Strynadka, N. C. J. and James, M. N. G. (**1988**) Proteins Struct. Funct. Genet. 3, 1-17!.

L29 ANSWER 10 OF 12 LIFESCI COPYRIGHT 2005 CSA on STN
ACCESSION NUMBER: 95:106843 LIFESCI
TITLE: Static **magnetic field** modulation of myosin phosphorylation: Calcium dependence in two enzyme

preparations
AUTHOR: Markov, M.S. [editor]; Pilla, A.A. [editor]; Miklavcic D. [editor]; Miklavcic D. [editor]; Karba R. [editor]; Vodovnik L. [editor]; Chiabrera A. [editor]
CORPORATE SOURCE: Bioelectrochem. Lab., Dep. Orthop., Mount Sinai Sch. Med., New York, NY 10029, USA
SOURCE: ADVANCES IN BIOELECTROMAGNETICS.;BIOELETROCHEM. BIOENERGET. , (1994) pp. 57-61;vol. 35, no. 1-2.
Meeting Info.: Proceedings of the Second Congress of the European Bioelectromagnetics Association. [np]. 9-11 Dec 1993.
ISSN: 0302-4598.
DOCUMENT TYPE: Journal
TREATMENT CODE: Conference
FILE SEGMENT: T
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The effects of weak, environmental range, static (d.c.) **magnetic fields** on myosin light chain phosphorylation in two enzyme preparations are reported. Specifically, the proposal that sensitivity to microtesla-level **magnetic fields** may be related to Ca super(2+) ion **binding** is examined using both myosin light chain kinase and **protein** kinase C assays. The electromagnetic field exposure system allowed **spatial** control of the applied static **magnetic field** in the 0.1-200 mu T range in the absence of a.c. components above plus or minus 0.1 mu T. The results showed that phosphorylation strongly depends on calcium ion concentration in the reaction mixture. Of interest is the observation that the **magnetic field** effect is maximal at low Ca super(2+) concentration for the calmodulin assay, whereas high Ca super(2+) concentration is required for the **protein** kinase C assay.

L29 ANSWER 11 OF 12 LIFESCI COPYRIGHT 2005 CSA on STN
ACCESSION NUMBER: 91:80975 LIFESCI
TITLE: Active site spectral studies on manganese superoxide dismutase.
AUTHOR: Whittaker, J.W.; Whittaker, M.M.
CORPORATE SOURCE: Dep. Chem., Carnegie Mellon Univ., 4400 Fifth Ave., Pittsburgh, PA 15213, USA
SOURCE: J. AM. CHEM. SOC., (1991) vol. 113, no. 15, pp. 5528-5540.
DOCUMENT TYPE: Journal
FILE SEGMENT: L; J
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Manganese superoxide dismutase from Escherichia coli has been prepared in homogeneous Mn super(3+) and Mn super(2+) redox forms for characterization by a combination of optical absorption, circular dichroism (CD), magnetic circular dichroism (MCD), and EPR spectroscopies. MCD spectra of the unliganded Mn super(3+) **protein** displays a strikingly simple pattern, a pair of bands of equal **magnitude** but oppositely signed intensity. Saturation magnetization curves for the native Mn site show a dramatic nesting that reflects large splittings in the paramagnetic ground state, suggesting positive zero-field splitting (D > 0). The ground-state behavior and the excited-state spectra can be interpreted in terms of a distorted trigonal-bipyramidal environment for the metal ion. **Binding** exogenous ligands (F super(-), N sub(3) super(-)) perturbs the Mn super(3+) site, leading to a distinctly different pattern of MCD intensity, a pseudo-A-term feature at high energy that exhibits a strong **magnetic field** saturation at low temperature. Saturation magnetization curves for the anion complexes are less broadly nested than for the native enzyme and appear to arise from a rhombically split non-Kramers doublet lowest in the quinlet ground state (D < 0).

L29 ANSWER 12 OF 12 LIFESCI COPYRIGHT 2005 CSA on STN

ACCESSION NUMBER: 82:13035 LIFESCI
TITLE: Direct Observations of the super(43)Ca NMR Signals From Ca super(2+) Ions **Bound** to **Proteins**.
AUTHOR: Andersson, T.; Drakenberg, T.; Forsen, S.; Thulin, E.; Swaerd, M.
CORPORATE SOURCE: Dep. Physical Chem. 1, Chem. Cent., Univ. Lund, S-220 07, Sweden
SOURCE: J. AM. CHEM. SOC., (1982) vol. 104, no. 2, pp. 576-580.
DOCUMENT TYPE: Journal
FILE SEGMENT: T
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The super(43)Ca NMR signals from Ca super(2+) ions **bound** to the Ca super(2+) **binding proteins** parvalbumin, troponin C, and calmodulin have been observed. The observation was made possible through the combined use of isotopically enriched super(43)Ca super(2+), FT techniques, high **magnetic fields**, and a solenoid type of probe design. Measurements of the apparent longitudinal relaxation rate, R sub(1), and the transverse relaxation rate, R sub(2), provide values of both the quadrupole coupling constant and the correlation time. The **magnitude** of the calculated correlation times is in good agreement with the rotational correlation time for the entire **protein** molecules, indicating the Ca super(2+)-**binding** sites to have a comparatively rigid structure.

=> (swing or spatial or remant or coercive or magnitude) and (magnetic or magnetism) and (target or DNA or RNA or protein or peptide) and (binding or bind or bound) and (ferro or magnetic)
L30 2 FILE AGRICOLA
L31 158 FILE BIOTECHNO
L32 0 FILE CONFSCI
L33 0 FILE HEALSAFE
L34 0 FILE IMSDRUGCONF
L35 36 FILE LIFESCI
L36 0 FILE MEDICONF
L37 62 FILE PASCAL

TOTAL FOR ALL FILES
L38 258 (SWING OR SPATIAL OR REMANT OR COERCIVE OR MAGNITUDE) AND (MAGNETIC OR MAGNETISM) AND (TARGET OR DNA OR RNA OR PROTEIN OR PEPTIDE) AND (BINDING OR BIND OR BOUND) AND (FERRO OR MAGNETIC)

=> magnetic(5A)(antigen or antibody)(10A)(isolation or isolating or separate or separation)
L39 10 FILE AGRICOLA
L40 47 FILE BIOTECHNO
L41 3 FILE CONFSCI
L42 1 FILE HEALSAFE
L43 0 FILE IMSDRUGCONF
L44 35 FILE LIFESCI
L45 0 FILE MEDICONF
L46 46 FILE PASCAL

TOTAL FOR ALL FILES
L47 142 MAGNETIC(5A)(ANTIGEN OR ANTIBODY)(10A)(ISOLATION OR ISOLATING OR SEPARATE OR SEPARATION)

=> l47 and probe and complex
L48 0 FILE AGRICOLA
L49 0 FILE BIOTECHNO
L50 0 FILE CONFSCI
L51 0 FILE HEALSAFE
L52 0 FILE IMSDRUGCONF

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L53           1 FILE LIFESCI
L54           0 FILE MEDICONF
L55           0 FILE PASCAL

TOTAL FOR ALL FILES
L56           1 L47 AND PROBE AND COMPLEX

=> d l56 ibib abs total

L56  ANSWER 1 OF 1  LIFESCI    COPYRIGHT 2005 CSA on STN
ACCESSION NUMBER:   96:110761  LIFESCI
TITLE:              Rapid detection of Mycobacterium avium in stool samples
                    from AIDS patients by immunomagnetic PCR
AUTHOR:             Li, Zhongming; Bai, G.H.; Von-Reyn, C.F.; Marino, P.;
                    Brennan, M.J.; Gine, N.; Morris, S.L.*
CORPORATE SOURCE:   FDA/CBER (HFM-431), 8800 Rockville Pike, Bethesda, MD
                    20892, USA
SOURCE:             J. CLIN. MICROBIOL., (1996) vol. 34, no. 8, pp. 1903-1907.
                    ISSN: 0095-1137.
DOCUMENT TYPE:      Journal
FILE SEGMENT:       J; V; A
LANGUAGE:           English
SUMMARY LANGUAGE:   English
AB   Direct PCR detection of bacteria in clinical samples is often hindered by
     the presence of compounds that inhibit the PCR. To improve and accelerate
     the diagnosis of Mycobacterium avium-M. intracellulare complex
     infections, an immunomagnetic PCR (IM-PCR) assay was developed. This
     IM-PCR procedure combines the separation of mycobacteria by
     antimycobacterial monoclonal antibody coupled to
     magnetic beads with an M. avium-M. intracellulare complex
     -specific PCR protocol based on 16S rRNA gene sequences. As few as 10 M.
     avium bacilli were detected in spiked human stool samples, a clinical
     specimen usually refractory to conventional PCR analysis, by the IM-PCR
     method. Moreover, M. avium organisms were detected in about 24 h in 18 of
     22 culture-confirmed fecal samples from AIDS patients. This IM-PCR
     protocol should allow for the rapid and sensitive detection of M. avium
     isolates in clinical specimens.


=> l47 and complex
L57           1 FILE AGRICOLA
L58           6 FILE BIOTECHNO
L59           0 FILE CONFSCI
L60           0 FILE HEALSAFE
L61           0 FILE IMSDRUGCONF
L62           4 FILE LIFESCI
L63           0 FILE MEDICONF
L64           6 FILE PASCAL

TOTAL FOR ALL FILES
L65          17 L47 AND COMPLEX

=> dup rem
ENTER L# LIST OR (END):l65
DUPLICATE IS NOT AVAILABLE IN 'IMSDRUGCONF, MEDICONF'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L65
L66            9 DUP REM L65 (8 DUPLICATES REMOVED)

=> d 166 ibib abs total

L66   ANSWER 1 OF 9  PASCAL  COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED. on
      STN
ACCESSION NUMBER:        2002-0391627   PASCAL
```

TITLE (IN ENGLISH): A chemiluminescence fiber-optic biosensor coupled with immunomagnetic separation for rapid detection of E. coli O157:H7
AUTHOR: YE J.; LIU Y.; LI Y.
CORPORATE SOURCE: Department of Poultry Science, University of Arkansas, Fayetteville, Arkansas, United States; Department of Biological and Agricultural Engineering, University of Arkansas, Fayetteville, Arkansas, United States
SOURCE: Transactions of the ASAE, (2002), 45(2), 473-478, 27 refs.
ISSN: 0001-2351 CODEN: TAAEAJ
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-2869, 354000108184910240
AN 2002-0391627 PASCAL

AB A biosensor, consisting of a chemiluminescence reaction cell, a fiber-optic light guide, and a luminometer linked to a PC, was developed in conjunction with immunomagnetic separation for rapid detection of E. coli O157:H7. The sample containing E. coli O157:H7 was first incubated with anti-E. coli O157:H7 coated magnetic beads and horseradish peroxidase (HRP) labeled anti-E. coli O157:H7 antibodies to form antibody-coated bead - bacteria - HRP-labeled **antibody** sandwich **complexes**. Then, a **magnetic** field was applied to **separate** the sandwich **complexes** from the sample, and the HRP in the **complexes** catalyzed the reaction of luminol and H.sub.2O.sub.2 in the reaction cell. The cell number of E. coli O157:H7 was determined by collecting the HRP-catalyzed chemiluminescence signal from the bead surface though a fiber-optic light guide and measuring the signal with a luminometer. Key parameters for the biosensor, such as magnetic bead volume, HRP-labeled antibody concentration, incubation time, and blocking agent, were determined for optimum operation conditions. The chemiluminescence biosensor was selective to E. coli O157:H7 in the presence of other bacteria in the sample, including Salmonella typhimurium, Campylobacter jejuni, and Listeria monocytogenes. The detection limit of the biosensor was 1.8 x 10.sup.2 CFU/mL, and the chemiluminescence signal ranged from 3.8 to 241.0 mV, corresponding to E. coli O157:H7 cells from 1.8 x 10.sup.2 to 4.5 x 10.sup.5 CFU/mL. A regression model with R.sup.2 = 0.958 was established for a calibration curve over the detection range. The biosensing procedure was simple and rapid, and could be completed within 1.5 h.

L66 ANSWER 2 OF 9 PASCAL on STN
ACCESSION NUMBER: 2002-0518998 PASCAL
TITLE (IN ENGLISH): Evaluation and optimization of a laboratory-constructed flow chamber for on-line immunomagnetic separation
AUTHOR: KARNES H. T.; TANG Z.
CORPORATE SOURCE: Department of Pharmaceutics Medical College of Virginia Virginia Commonwealth University, Richmond, VA 23298-0533, United States
SOURCE: Instrumentation Science and Technology, (2002), 30(3), 295-309, 29 refs.
ISSN: 1073-9149
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-14080

AN 2002-0518998 PASCAL
AB Immunomagnetic **separation** (IMS) uses **magnetic** beads to facilitate **separation** of **antibody**-bound labeled antigens from free antigens in solution. Off-line immunomagnetic separation is time consuming due to the requirement of washing the magnetizable beads between assays and the multiple steps involved in the separation process. On-line IMS, in the flow injection mode, can overcome the disadvantages of off-line IMS, such as multiple washing steps. The purpose of this work is to develop, optimize, and validate an on-line magnetic separation flow chamber in the flow injection mode, suitable for post-column immunoreaction detection. The ends of the flow chamber were connected to the flow injection system. The on-line magnetic flow chamber was constructed using 1.0 I.D. x 1.58 O.D.mm Teflon tubing that was attached to an electromagnet. The electromagnet was constructed by wrapping a 305 x 25 x 40 mm block of hard steel with fine copper wire which was supplied with direct current (dc). The magnetic field was applied and released by switching the power on and off. The electromagnet was designed to have three terminals with 750 turns (yellow), 1000 turns (blue) and 1250 turns (red), respectively, to generate three different electromagnetic fields. A cooling tube was wound among the copper wire and ice water was used to cool down the core of the electromagnet. Water was pumped into the cooling tube using a VWR peristaltic pump and circulated in a forty-gallon container full of ice water. Various orientations and volumes of the flow chamber, various flow rates, and currents were investigated to obtain the maximum magnetic trapping efficiency. Digoxin was selected as a model analyte and a competitive format was used for immunoassay. Digoxigenin was labeled with R-phycoerythrin (PE-D) as a competing labeled antigen and anti-digoxin antibodies covalently linked biotin through streptavidin coated magnetic beads were used for magnetic separation. The immunoassay mixture was injected into the flow chamber after immunoreaction and immunomagnetic **complexes** were captured on the wall of the flow chamber using the electromagnet. The maximum trapping efficiency obtained was 98% using a five-fold straight flow chamber at a flow rate of 0.5 mL/min and a current of 1.5 amperes (A). The on-line magnetic separation immunoassay of digoxin in spiked phosphate buffer demonstrated a dynamic range of 0.5-15 ng/mL. A quadratic fit was found to provide the best fit to the data (r = 0.9937). The precision for two controls, 4.0 and 12 ng/mL, were 14.05% RSD and 10.75% RSD (n = 6) and the accuracy was 5.8% and 3.31% (n = 6), respectively. The limit of detection was calculated to be 0.44 ng/mL.

L66 ANSWER 3 OF 9 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
DUPLICATE
ACCESSION NUMBER: 2002:34450733 BIOTECHNO
TITLE: Immunomagnetic separation reagents as markers in electron microscopy
AUTHOR: Fisher P.J.; Springett M.J.; Dietz A.B.; Bulur P.A.; Vuk-Pavlovic S.
CORPORATE SOURCE: P.J. Fisher, Department of Biochemistry, Mayo Clinic, 200 First St. SW, Rochester, MN 55905, United States. E-mail: fisher.phyllis@mayo.edu
SOURCE: Journal of Immunological Methods, (01 APR 2002), 262/1-2 (95-101), 17 reference(s)
CODEN: JIMMBG ISSN: 0022-1759
PUBLISHER ITEM IDENT.: S0022175902000078
DOCUMENT TYPE: Journal; Article
COUNTRY: Netherlands
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2002:34450733 BIOTECHNO
AB **Antibodies** coupled to **magnetic** particles have been employed for immunomagnetic cell **isolation**, but their consequent use for electron microscopy (EM) has not been evaluated. We

used commercial antibodies coupled to iron-dextran to isolate T cells and monocytes/macrophages by immunomagnetic adsorption from normal human peripheral blood mononuclear cells. Subsequently, we studied the association of electron-dense immunomagnetic reagents with cell membranes. CD14-positive monocytes/macrophages isolated from fixed peripheral blood mononuclear cells retained electron-dense beads on the plasma membrane, while live cells internalized them. Flow cytometry and electron microscopy measurements of the percentage of cells that bound a CD4-specific immunomagnetic reagent in pan-T cell isolates (containing numerous T cell subtypes) were indistinguishable. The immunomagnetic reagent associated with cells could be secondarily labeled by secondary antibody coupled to colloidal gold. This study shows that these reagents used for cell isolation or just labeling, remain associated with their targets at the cell membrane. Immunomagnetic reagents allow "capturing" of rare cells from **complex** mixtures, purifying and concentrating them in a single step for subsequent electron microscopy. The large number of commercially available immunomagnetic reagents specific for different human, mouse and rat antigens provides additional resources for visualization of cellular ultrastructure. .COPYRGT. 2002 Elsevier Science B.V. All rights reserved.

L66 ANSWER 4 OF 9 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 2001-0468248 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2001 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): Immunomagnetic isolation and long-term culture of mouse type A spermatogonia
AUTHOR: VAN DER WEE Kathy S.; JOHNSON Eric W.; DIRAMI Ghenima; DYM Martin; HOFMANN Marie-Claude
CORPORATE SOURCE: Department of Biology, The University of Dayton, Dayton, Ohio, United States; Department of Cell Biology, Georgetown University Medical Center, Washington, DC, United States
SOURCE: Journal of andrology, (2001), 22(4), 696-704, 27 refs. ISSN: 0196-3635 CODEN: JOAND3
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-18896, 354000096616470220

AN 2001-0468248 PASCAL
CP Copyright .COPYRGT. 2001 INIST-CNRS. All rights reserved.
AB In the mammalian testis, type A spermatogonia proliferate and differentiate into sperm under the tight control of both endocrine and paracrine factors. In order to study the **complex** process of spermatogenesis at the molecular level, an in vitro system must be devised in which type A spermatogonia can be cultured for a prolonged period of time. Therefore, cocultures including type A spermatogonia and Sertoli cells, which act as nurse cells to the developing germ cells, are desirable. We have developed a method for the specific **isolation** of type A spermatogonia using **magnetic** beads and **antibodies** that recognize the c-kit receptor or the homophilic adhesion molecule, Ep-CAM. Purified spermatogonia could survive for a period of 25 days when cocultivated on Sertoli cell monolayers. Moreover, we recently established Sertoli cell lines that produce growth factors that are essential for the maintenance of spermatogonia in a proliferative state. Some of these Sertoli cell lines are able to reorganize into tubular structures when cultivated on a layer of Matrigel as extracellular matrix. We show here that type A spermatogonia associate specifically with the Sertoli cell tubules, and are able to replicate their DNA in this environment. Thus, these in vitro culture systems could be used for the long-term culture of primary, nonimmortalized type A spermatogonia.

L66 ANSWER 5 OF 9 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 1997:27463270 BIOTECHNO
TITLE: Study of T-lymphocyte subsets of healthy and Mycobacterium avium subsp. paratuberculosis-Infected cattle
AUTHOR: Bassey E.O.E.; Collins M.T.
CORPORATE SOURCE: E.O.E. Bassey, Dept. of Medicine-Infectious Dis., Wishard Memorial Hospital, Indiana University, 1001 West Tenth St., Indianapolis, IN 46202-2879, United States.
SOURCE: Infection and Immunity, (1997), 65/11 (4869-4872), 19 reference(s)
CODEN: INFIBR ISSN: 0019-9567
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 1997:27463270 BIOTECHNO
AB The relative contributions of T-lymphocyte subsets to host defense in cattle infected with Mycobacterium avium subsp. paratuberculosis is reported. The subsets were purified with appropriate monoclonal **antibodies** and a **magnetic** bead column **separation** system, and their purity was verified by flow cytometry. Biological activity of each subset, expressed as lymphoproliferation and gamma interferon (IFN-γ) production, was measured in response to phytohemagglutinin (PHA) and an M. avium antigen preparation (A- PPD). IFN-γ was measured by antibody capture enzyme-linked immunosorbent assay. The results showed a correlation between proliferation and IFN-γ production in response to A-PPD but not to PHA. In response to PHA, CD4.sup.+ lymphocytes were the most prolific producers of IFN-γ. CD8.sup.+ lymphocytes produced IFN-γ, to a lesser extent, whereas γδ.sup.+ T lymphocytes produced little or no IFN-γ. Differences observed between the amount of IFN-γ produced by CD4.sup.+ versus CD8.sup.+ cells and CD4.sup.+ versus γδ.sup.+ cells were significant ($P < 0.01$), but those between peripheral blood mononuclear cells (PBMC) and CD4.sup.+ T cells were not. Similar responses to A-PPD were observed except that PBMC produced higher levels of IFN-γ than did CD4.sup.+ T cells. These data for cattle are similar to observations made for other animal species, where CD4.sup.+ cells are the major type of T lymphocytes producing IFN- γ. They further suggest that whatever the role γδ.sup.+ T cells may play in paratuberculosis, it is not likely to be mediated by IFN-γ, production.

L66 ANSWER 6 OF 9 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
DUPLICATE
ACCESSION NUMBER: 1997:27179618 BIOTECHNO
TITLE: Combined immmunomagnetic cell sorting and ELISPOT assay for the phenotypic characterization of specific antibody-forming cells
AUTHOR: Lakew M.; Nordstrom I.; Czerkinsky C.; Quiding-Jarbrink M.
CORPORATE SOURCE: M. Quiding-Jarbrink, Dept. Med. Microbiology/Immunology, University of Goteborg, Guldhedsgatan 10A, S-413 46 Goteborg, Sweden. E-mail: quidingj@mailer.mednet.gu.se
SOURCE: Journal of Immunological Methods, (1997), 203/2 (193-198), 16 reference(s)
CODEN: JIMMBG ISSN: 0022-1759
PUBLISHER ITEM IDENT.: S0022175997000306
DOCUMENT TYPE: Journal; Article
COUNTRY: Netherlands
LANGUAGE: English

their use for immunomagnetic capture of spores from soil.
AUTHOR(S): Wipat, A.; Wellington, E.M.H.; Saunders, V.A.
CORPORATE SOURCE: University of Newcastle upon Tyne, Newcastle, UK
AVAILABILITY: DNAL (QR1.J64)
SOURCE: Microbiology, Aug 1994. Vol. 140, No. pt.8. p. 2067-2076
Publisher: Reading, U.K. : Society for General Microbiology, c1994-
CODEN: MROBEO; ISSN: 1350-0872
NOTE: Includes references
PUB. COUNTRY: England; United Kingdom
DOCUMENT TYPE: Article
FILE SEGMENT: Non-U.S. Imprint other than FAO
LANGUAGE: English

AB Monoclonal antibodies were produced to Streptomyces lividans spore surface antigens. One particular hybridoma cell line, 43H6, produced a monoclonal antibody that reacted exclusively with Streptomyces cluster group 21 in an enzyme-linked immunosorbent assay (ELISA). Antibody 43H6 was found to be of subclass IgG1, kappa light chain. Western blot (immunoblot) analysis revealed that 43H6 recognized a major outer spore polypeptide of about 37 000 Da. The epitope was stably maintained in S. lividans spores over at least seven sporulation cycles on laboratory medium and for at least 14 weeks in sterile soil systems. The species group specificity of antibody 43H6 was exploited in the development of an immunocapture technique for the **isolation** of streptomycetes from soil. **Magnetic** beads coated with **antibody** 43H6 were mixed with soil samples seeded with S. lividans spores. Spore-bead **complexes** were recovered using magnets. Treatment of beads with blocking agents and the inclusion of detergents in the recovery system lessened non-specific binding of spores to beads and improved recovery. In buffer solutions decreasing the spore concentration increased the recovery values for a fixed bead concentration. At a spore concentration of 5 X 10(7) ml-1 the recovery was 4.3% whilst at 5 X 10(7) ml-1 it was 76% for a fixed bead concentration of 0.6 mg ml-1. Using a bead concentration of 2 mg per 10(9) soil, approximately 30% of the target spore population of 10(6) c.f.u. was recovered from sterile soil and 4% from non-sterile soil. This method offers a rapid means of selectively recovering and concentrating Streptomyces spores from soil samples.

L66 ANSWER 9 OF 9 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 1991:22008291 BIOTECHNO
TITLE: Analysis and **isolation** of human transferrin receptor using the OKT-9 monoclonal **antibody** covalently crosslinked to **magnetic** beads
AUTHOR: Karlsson G.B.; Platt F.M.
CORPORATE SOURCE: Glycobiology Unit, Department of Biochemistry, University of Oxford, South Parks Road, Oxford OX1 3QU, United Kingdom.
SOURCE: Analytical Biochemistry, (1991), 199/2 (219-222)
CODEN: ANBCA2 ISSN: 0003-2697
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 1991:22008291 BIOTECHNO

AB A method is described for the use of magnetic beads as a solid phase for the immunoprecipitation of labeled proteins. The anti-human transferrin receptor monoclonal antibody OKT-9 has been coupled to sheep anti-mouse IgG1- coated magnetic beads using the crosslinking agent dimethyl pimelimidate. The transferrin receptor is readily detected by sodium dodecyl sulfate- polyacrylamide gel electrophoresis and autoradiography following immunoprecipitation from .sup.3.sup.5S-labeled cell lysates. When compared with precipitations using OKT-9 coupled to protein G

Sepharose the magnetic beads result in fewer nonspecific bands. The protocol described is generally applicable to the identification of labeled proteins. In addition, because magnetic beads are amenable to covalent crosslinking procedures they can be used for the purification of proteins from **complex** mixtures. Covalently crosslinked OKT-9 sheep anti-mouse IgG1-coated magnetic beads have been used to affinity purify unlabeled transferrin receptor from cell lysates giving comparable purity and yield to transferrin Sepharose isolated transferrin receptor. The major advantages offered by magnetic beads compared to conventional affinity matrices are low nonspecific binding and the rapidity with which the purification can be performed.

=> ((magnetic bead) or (magnetic particle)) and (swing or remant or coercive or magnitude) and complex
L67 0 FILE AGRICOLA
L68 0 FILE BIOTECHNO
L69 0 FILE CONFSCI
L70 0 FILE HEALSAFE
L71 0 FILE IMSDRUGCONF
L72 0 FILE LIFESCI
L73 0 FILE MEDICONF
L74 17 FILE PASCAL

TOTAL FOR ALL FILES
L75 17 ((MAGNETIC BEAD) OR (MAGNETIC PARTICLE)) AND (SWING OR REMANT OR COERCIVE OR MAGNITUDE) AND COMPLEX

=> l75 and probe
L76 0 FILE AGRICOLA
L77 0 FILE BIOTECHNO
L78 0 FILE CONFSCI
L79 0 FILE HEALSAFE
L80 0 FILE IMSDRUGCONF
L81 0 FILE LIFESCI
L82 0 FILE MEDICONF
L83 0 FILE PASCAL

TOTAL FOR ALL FILES
L84 0 L75 AND PROBE

=> l75 and (antibody or antigen or DNA or RNA or protein)
L85 0 FILE AGRICOLA
L86 0 FILE BIOTECHNO
L87 0 FILE CONFSCI
L88 0 FILE HEALSAFE
L89 0 FILE IMSDRUGCONF
L90 0 FILE LIFESCI
L91 0 FILE MEDICONF
L92 0 FILE PASCAL

TOTAL FOR ALL FILES
L93 0 L75 AND (ANTIBODY OR ANTIGEN OR DNA OR RNA OR PROTEIN)

=> l74 and (protein or antigen or antibody or bind or bound or DNA or RNA or nucleic)
L94 0 FILE AGRICOLA
L95 0 FILE BIOTECHNO
L96 0 FILE CONFSCI
L97 0 FILE HEALSAFE
L98 0 FILE IMSDRUGCONF
L99 0 FILE LIFESCI
L100 0 FILE MEDICONF
L101 0 FILE PASCAL

TOTAL FOR ALL FILES
L102 0 L74 AND (PROTEIN OR ANTIGEN OR ANTIBODY OR BIND OR BOUND OR DNA OR RNA OR NUCLEIC)

=> dup rem
ENTER L# LIST OR (END):l75
DUPLICATE IS NOT AVAILABLE IN 'IMSDRUGCONF, MEDICONF'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L75
L103 17 DUP REM L75 (0 DUPLICATES REMOVED)

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L103 ANSWER 1 OF 17 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 2003-0240870 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2003 American Institute of Physics. All rights reserved.
TITLE (IN ENGLISH): Electromagnetic and magnetic properties of multicomponent metal oxides heterostructures: Nanometer versus micrometer-sized particles
AUTHOR: BROSSEAU Christian; YOUSSEF Jamal Ben; TALBOT Philippe; KONN Anne-Marie
CORPORATE SOURCE: Laboratoire d<right single quotation mark>Electronique et Systemes de Telecommunications (UMR 6165 CNRS), Universite de Bretagne Occidentale, 6 Avenue Le Gorgeu, 29285 Brest Cedex, France; Laboratoire de Magnetisme de Bretagne (UMR 6165 CNRS), Universite de Bretagne Occidentale, 6 Avenue Le Gorgeu, 29285 Brest Cedex, France; Laboratoire d<right single quotation mark>Electronique et Systemes de Telecommunications, Universite de Bretagne Occidentale, 6 Avenue Le Gorgeu, 29285 Brest Cedex, France
SOURCE: Journal of applied physics, (2003-06-01), 93(11), 9243-9256
ISSN: 0021-8979 CODEN: JAPIAU
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-126
AN 2003-0240870 PASCAL
CP Copyright .COPYRGT. 2003 American Institute of Physics. All rights reserved.
AB We have measured the composition and frequency-dependent **complex** effective permittivities and permeabilities in zero applied field of a series of ZnO and ferrimagnetic γ-Fe.sub.2 O.sub.3 composites prepared by powder pressing. The overall features of the room temperature electromagnetic properties of these diluted magnetic semiconductor composites exhibit a strong dependence on the powder size of the starting materials. For instance, electromagnetic spectroscopy over the frequency range (300 MHz-10 GHz) shows that composites made of nanoparticles (N-type samples) display a strong increase of the real and imaginary parts of the permeability compared to composites made of micron-sized particles (M-type samples). The observed dielectric behavior as a function of composition is manifestly at odds with the predictions from the simple property-averaging continuum model of Bruggeman. Additionally, a gyromagnetic resonance in the gigahertz region of frequency has been established for N-type samples which is not observable in M-type samples. Examination of the dynamics of the magnetization distribution in N-type samples shows that the usual Landau-Lifshitz-Gilbert (LLG) equation can represent satisfactorily the gyromagnetic resonance line. Two important features of the data are the slight increase of the resonance frequency

and the more important decrease of the width at half height of the gyromagnetic resonance line as the content of the magnetic phase is increased. It appears also that the value of the damping constant, characterizing the dynamics of magnetization, extracted from the fit of the gyromagnetic resonance line is consistent with previous experimental determinations. We attribute the remaining deviations in the fit and the discrepancies in the damping constant estimates namely to two approximations in our approach. First, the mean-field model considered here neglects composition fluctuations. Another source of the corrections are those due to the polydispersity of the nanoparticles. In contrast to the permittivity results, the comparison of the experimental values of the effective permeability, as a function of composition, with the analytical model combining the LLG and Bruggeman equations shows a good agreement. Given that the volume fraction of the organic binder has an effect on the shape of the gyromagnetic resonance line, we investigate also how this parameter affects the characteristics of the resonance mode. The analysis of the hysteretic behavior of these multiphase granular materials at room temperature indicates that the coercivity and the saturation magnetization normalized to the content of Fe.sub.2O.sub.3 in the sample is strongly dependent on particle size, but remain practically constant over the entire Fe.sub.2O.sub.3 volume fraction range investigated. Furthermore, the reduced remanence ratio is found much smaller than the Stoner and Wohlfarth<right single quotation mark>s prediction concerning randomly distributed single domain particles without interaction. Possible origins for this difference have been analyzed. The suggestion, through Chen <et al.><right single quotation mark>s analysis [C. Chen, O. Kitakami, and Y. Shimada, J. Appl. Phys. 84, 2184 (1988)], that the surface anisotropy is responsible for the coercivity behavior is quantitatively consistent with the experimental data concerning N-type samples. .COPYRGT. 2003 American Institute of Physics.

L103 ANSWER 2 OF 17 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 2003-0453190 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2003 American Institute of Physics. All rights reserved.
TITLE (IN ENGLISH): Hexaferrite-FeCo nanocomposite particles and their electrical and magnetic properties at high frequencies
AUTHOR: SUDAKAR C.; SUBBANNA G. N.; KUTTY T. R. N.
CORPORATE SOURCE: Materials Research Centre, Indian Institute of Science, Bangalore 560012, India
SOURCE: Journal of applied physics, (2003-11-01), 94(9), 6030-6033
ISSN: 0021-8979 CODEN: JAPIAU
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-126

AN 2003-0453190 PASCAL
CP Copyright .COPYRGT. 2003 American Institute of Physics. All rights reserved.
AB Nanocomposites are realized by chemical reduction whereby the conducting **magnetic particles** of Fe-Co alloy are generated within the insulating ferrimagnetic BaCo.sub.2Fe.sub.1.sub.6O.sub.2.sub.7 or Ba.sub.2Co.sub.2Fe.sub.1.sub.2O.sub.2.sub.2 hexaferrite matrix. Transmission electron microscopy revealed that metal nanoparticles precipitate coherently as thin flakes along the a-b planes of the derivative magnetoplumbite lattice of the hexaferrites above the characteristic reduction temperature, T.sub.R>375<hair thin space>°C in H.sub.2 atmosphere. The coercivity increases with T.sub.R in the early stages of the solid-state precipitation and then decreases with the formation of larger fractions of Fe-Co alloy; a

converse trend is noticed for magnetization. The **complex** permittivity increases with reduction to .eqvsim.50 in the broad frequency range of 4-18 GHz. The **complex** permeability is also enhanced with the content of Fe-Co nanoparticles. It is proposed that the spin reorientation at the Fe-Co/hexaferrite interface gives rise to broadband response, rendering these composite particles useful as electromagnetic microwave absorbers. .COPYRGT. 2003 American Institute of Physics.

L103 ANSWER 3 OF 17 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 2002-0243428 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2002 American Institute of Physics. All rights reserved.
TITLE (IN ENGLISH): New experimental method for Preisach distribution identification
AUTHOR: CERCHEZ M.; BISSELL P. R.; STANCU Al.
CORPORATE SOURCE: Alexandru Ioan Cuza University, Faculty of Physics, 11 Blvd. Copou, Iasi 6600, Romania; University of Central Lancashire, Centre for Materials Science, Preston, PR1 2HE, United Kingdom; Alexandru Ioan Cuza University, Faculty of Physics, 11 Blvd. Copou, Iasi 6600, Romania
SOURCE: Journal of applied physics, (2002-05-15), 91(10), 7654-7656
ISSN: 0021-8979 CODEN: JAPIAU
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-126
AN 2002-0243428 PASCAL
CP Copyright .COPYRGT. 2002 American Institute of Physics. All rights reserved.
AB A mixed (parametric/nonparametric) method to identify the Preisach distribution of particulate recording media is presented. The algorithm is tested on computer-generated data and is applied to Ba-Fe random oriented recording media. The results are in good agreement with the experimental data. We show that the Preisach distribution may not always be accurately described by analytical functions and that a discrete Preisach distribution could be used for better agreement between the simulations and the experimental data for **complex** magnetization processes. .COPYRGT. 2002 American Institute of Physics.

L103 ANSWER 4 OF 17 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 2002-0586828 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2002 American Institute of Physics. All rights reserved.
TITLE (IN ENGLISH): Preparation of Spinel-Type Ferrite Fine Particles via Plasma Route Using Amorphous Citrate Gel as a Precursor
AUTHOR: KIKUKAWA Nobuyuki; SUGASAWA Masami; KOBAYASHI Satoru
CORPORATE SOURCE: National Institute of Advanced Industrial Science and Technology (AIST), Tsukuba 305-8569, Japan
SOURCE: Japanese Journal of Applied Physics, Part I : Regular papers, short notes & review papers, (2002-10), 41(10), 5991-5992
ISSN: 0021-4922 CODEN: JAPNDE
DOCUMENT TYPE: Journal; Short communication
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-9959
AN 2002-0586828 PASCAL

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AB In order to prepare **complex** ferrite fine particles with good crystallinity and stoichiometry, the authors adopted amorphous citrate gel as the precursor for plasma powder synthesis. The produced particles were monophase spinel-type ferrites of M1-xZnxFe2O4 (M = Mn, Ni, Cu, x = 0.3 or 0.5) with good crystallinity. Energy-dispersive X-ray spectroscopy (EDX) microanalysis of the precursor and product particles (Mn-Zn-Fe-O) revealed very sharp distributions of the Mn/Fe ratio in both precursor and product. The average size of the fine particles was 51 nm, and the **coercive** forces were 45-71 Oe; these measurements suggest the suitability of these fine particles in applications utilizing the effects of magnetic heating due to hysteresis losses. .COPYRGT. 2002 The Japan Society of Applied Physics

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ACCESSION NUMBER: 2002-0430102 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2002 American Institute of Physics. All rights reserved.
TITLE (IN ENGLISH): Structural and magnetic characteristics of monodispersed Fe and oxide-coated Fe cluster assemblies
AUTHOR: PENG D. L.; HIHARA T.; SUMIYAMA K.; MORIKAWA H.
CORPORATE SOURCE: Department of Materials Science and Engineering, Nagoya Institute of Technology, Nagoya 466-8555, Japan
SOURCE: Journal of applied physics, (2002-09-15), 92(6), 3075-3083
ISSN: 0021-8979 CODEN: JAPIAU
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-126

AN 2002-0430102 PASCAL

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AB We systematically studied structural and magnetic characteristics of size- monodispersed Fe and oxide-coated Fe cluster assemblies with the mean cluster sizes of 7-16 nm. Transmission electron microscopy and scanning electron microscopy (SEM) observations show that the Fe clusters in the assemblies maintain their original size at room temperature. In the SEM images, a random stacking of the Fe clusters and a porous structure with a low cluster packing fraction of about 25% are observed. For the Fe cluster assemblies, magnetic coercivity (H.sub.c) at room temperature increases from 4 x 10.sup.1 to 4 x 10.sup.2 Oe by increasing the mean cluster size from 7.3 to 16.3 nm. Using the experimental values of the coercivity at T>=100 K and the fitting values of blocking temperature T.sub.B from H.sub.c=H.sub.c.sub.0[1-(T/T.sub.B).sup.1.sup./.sup.2], we estimated the values of magnetic anisotropy constant K of the order of 10.sup.6 erg/cm.sup.3 from T.sub.B=KV/25k.sub.B, which is larger by an order of **magnitude** than the bulk Fe value (5 x 10.sup.5 erg/cm.sup.3). Such a large effective anisotropy at T>=100 K is ascribed to the large surface anisotropy effects of the small clusters and the low cluster-packing fraction of the Fe cluster assemblies. For the oxide-coated Fe cluster samples, the coercivity strongly depends on the oxygen gas flow rate during deposition, cluster size, and temperature. In the case of a high oxygen gas flow rate (namely high surface-oxidized clusters), the ferrimagnetic oxide shell crystallites also affect the coercivity at T>50 K: The hysteresis loop shift disappears, leading to a **complex** change in the coercivity and an enhancement of the effective anisotropy constant. .COPYRGT. 2002 American Institute of Physics.

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ACCESSION NUMBER: 2002-0497630 PASCAL
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TITLE (IN ENGLISH): Magnetization orientation dependence of the quasiparticle spectrum and hysteresis in ferromagnetic metal nanoparticles
AUTHOR: CEHOVIN A.; CANALI C. M.; MACDONALD A. H.
CORPORATE SOURCE: Division of Solid State Theory, Department of Physics, Lund University, SE-223 62 Lund, Sweden; Department of Technology, Kalmar University, 391 82 Kalmar, Sweden; Division of Solid State Theory, Department of Physics, Lund University, SE-223 62 Lund, Sweden; Department of Physics, University of Texas at Austin, Austin, Texas 78712
SOURCE: Physical review. B, Condensed matter and materials physics, (2002-09-01), 66(9), 094430-094430-15 ISSN: 1098-0121 CODEN: PRBMDO
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-144 B
AN 2002-0497630 PASCAL
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AB We use a microscopic Slater-Koster tight-binding model with short-range exchange and atomic spin-orbit interactions that realistically captures generic features of ferromagnetic metal nanoparticles to address the mesoscopic physics of magnetocrystalline anisotropy and hysteresis in nanoparticle-quasiparticle excitation spectra. Our analysis is based on qualitative arguments supported by self-consistent Hartree-Fock calculations for nanoparticles containing up to 260 atoms. Calculations of the total energy as a function of magnetization direction demonstrate that the magnetic anisotropy per atom fluctuates by several percent when the number of electrons in the particle changes by 1, even for the largest particles we consider. Contributions of individual orbitals to the magnetic anisotropy are characterized by a broad distribution with a mean more than two orders of **magnitude** smaller than its variance and with no detectable correlations between anisotropy contribution and quasiparticle energy. We find that the discrete quasiparticle excitation spectrum of a nanoparticle displays a **complex** nonmonotonic dependence on an external magnetic field, with abrupt jumps when the magnetization direction is reversed by the field, explaining recent spectroscopic studies of magnetic nanoparticles. Our results suggest the existence of a broad crossover from a weak spin-orbit coupling to a strong spin-orbit coupling regime, occurring over the range from approximately 200- to 1000-atom nanoparticles.

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ACCESSION NUMBER: 2002-0256257 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2002 American Institute of Physics. All rights reserved.
TITLE (IN ENGLISH): Computational model of the magnetic and transport properties of interacting fine particles
AUTHOR: VERDES C.; RUIZ DIAZ B.; THOMPSON S. M.; CHANTRELL R. W.; STANCU Al.
CORPORATE SOURCE: Physics Department, Durham University, South Road, Durham DH1 3LE, United Kingdom; Physics Department, York University, Heslington, York YO10 5DD, United Kingdom; Physics Department, Durham University, South Road, Durham DH1 3LE, United Kingdom; Seagate

Research, River Park Commons, Suite 550, 2403 Sydney Street, Pittsburgh, Pennsylvania 15203-2116; Physics Department, University Al. Ioan Cuza, Iasi, Romania
SOURCE: Physical review. B, Condensed matter and materials physics, (2002-05-01), 65(17), 174417-174417-10
ISSN: 1098-0121 CODEN: PRBMDO
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-144 B
AN 2002-0256257 PASCAL

AB A computational model is applied to the study of the hysteresis properties of a system of interacting single domain particles. The model is based on Monte Carlo techniques and takes into account both magnetostatic and exchange interactions. The results presented concentrate on a detailed study of the behavior of Co particles, with the interaction strength varied by variations in the packing density. It is found that the magnetic properties are strongly dependent on the parameter β=KV/kT, with K the anisotropy constant and V the mean particle volume. For small β-i.e., close to superparamagnetic systems-the microstructure is dominated by a tendency to flux closure. However, the interactions lead to an increase in the local energy barriers, resulting in an increase in H.sub.c with packing density ε. For large β the anisotropy and magnetostatic interaction fields become comparable and the competition leads to a decrease in the coercivity H.sub.c with ε. For intermediate values of β a maximum in the variation of H.sub.c with ε is predicted. The irreversible susceptibility is shown to have a **complex** dependence on interactions, especially in small fields where frustration effects arising from the competition between exchange and magnetostatic interactions are apparent. Exchange and magnetostatic interactions give rise to local magnetic order which is strongly dependent on the relative strength of the exchange interactions. The magnetic order has a strong bearing on the magnetic properties. A link is also made to the transport properties of the system, which are dependent on a spin-spin correlation function. It is shown that exchange interactions give rise to a significant deviation from the quadratic dependence of the giant magnetoresistance on M.sup.2.

L103 ANSWER 8 OF 17 PASCAL on STN
ACCESSION NUMBER: 2001-0238389 PASCAL

TITLE (IN ENGLISH): Synthesis and magnetic properties of CoFe.sub.2O.sub.4 spinel ferrite nanoparticles doped with lanthanide ions
AUTHOR: KAHN Myrtil L.; ZHANG Z. John
CORPORATE SOURCE: School of Chemistry and Biochemistry, Georgia Institute of Technology, Atlanta, Georgia 30332-0400
SOURCE: Applied physics letters, (2001-06-04), 78(23), 3651-3653
ISSN: 0003-6951 CODEN: APPLAB
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-10020
AN 2001-0238389 PASCAL

AB Lanthanide ions have been doped into cobalt spinel ferrites using an oil-in-water micellar method to form CoLn.sub.0.sub...sub.1.sub.2Fe.sub.1 .sub...sub.8.sub.8O.sub.4 nanoparticles with Ln=Ce, Sm, Eu, Gd, Dy, or Er. Doping with lanthanide ions (Ln.sup.I.sup.I.sup.I) modulates the magnetic properties of cobalt spinel ferrite nanoparticles. In particular cases of Gd.sup.3.sup.+ or Dy.sup.3.sup.+ ions, a dramatic increase in the blocking temperature and coercivity is observed. Indeed, the introduction of only 4% of Gd.sup.3.sup.+ ions increases the blocking temperature .eqvsim.100 K and the coercivity 60%. Initial studies on the magnetic properties of these doped nanoparticles clearly demonstrate that the relationship between the modulation of magnetic properties and the nature of doped Ln.sup.I.sup.I.sup.I ions is interesting but very **complex**. .COPYRGT. 2001 American Institute of Physics.

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ACCESSION NUMBER: 2002-0016770 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2002 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): On the Cox-Merz rule for magnetic dispersions
AUTHOR: CHAE Byeong S.; LANE Alan M.; WIEST John M.
CORPORATE SOURCE: Department of Chemical Engineering and Center for Materials for Information Technology, University of Alabama, Tuscaloosa, AL 35487-0203, United States
SOURCE: Rheologica acta, (2001), 40(6), 599-602, 10 refs.
ISSN: 0035-4511 CODEN: RHEAAK
DOCUMENT TYPE: Journal; Short communication
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: Germany, Federal Republic of
LANGUAGE: English
AVAILABILITY: INIST-1862, 354000096273170100
AN 2002-0016770 PASCAL
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AB The Cox-Merz rule can be a useful, empirical tool for relating steady and oscillatory shear flow property measurements. Here we test its applicability for magnetic dispersions. Neither the rule nor a previously published modification of it applies for the dispersions, but we demonstrate that the steady shear viscosity and the **magnitude** of the **complex** viscosity are nonetheless related

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ACCESSION NUMBER: 2001-0301828 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2001 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): Magnetic applications of polymer gels
Polymer-solvent **complexes** and intercalates : Besancon, 28-30 August 2000
AUTHOR: LOPEZ Daniel; CENDOYA Lone; MIJANGOS Carmen; JULIA Anna; ZIOLO Ron; TEJADA Javier
GUENET Jean-Michel (ed.)
CORPORATE SOURCE: Insituto de Ciencia y Tecnologia de Polimeros, CSIC, c/ Juan de la Cierva 3, 28006 Madrid, Spain; Laboratori UBX, Avinguda Diagonal 647, 08028 Barcelona, Spain
SOURCE: Makromolekulare Chemie (Die). Macromolecular symposia, (2001), 166, 173-178, 16 refs.
Conference: 3 International conference on polymer-solvent complexes and intercalates, Besancon (France), 28 Aug 2000
ISSN: 0258-0322
ISBN: 3-527-30328-6
DOCUMENT TYPE: Journal; Conference
BIBLIOGRAPHIC LEVEL: Analytic

COUNTRY: Switzerland
LANGUAGE: English
AVAILABILITY: INIST-4111 S, 354000092390970180
AN 2001-0301828 PASCAL
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AB In this paper we report results of both, material preparation and magnetic characterisation, on CoFe.sub.2O.sub.4 particles of nanometric size formed by in-situ precipitation within polymer gels. The size of the particles was controlled within a very narrow volume distribution and its average value was shifted from 2 to 10 nm. The existence of nanoparticles showing, at room temperature, **coercive** field values between 500 and 900 Oe and saturation magnetisations of about 500 emu/cm.sup.3, suggest to use these systems to get magnetic recording media with ultra high density. Poly(vinyl alcohol)(PVA) and Polystyrene (PS) films were prepared from this nanocomposite material. After a magnetic field treatment nanoparticles within the PVA films are free to rotate in response to an applied magnetic field. This PVA based nanocomposite film portends a new class of magnetic material with very little or no electrical and magnetic loss.

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ACCESSION NUMBER: 2001-0184094 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2001 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): Formation of nickel dispersed carbon spheres from chelate resin and their magnetic properties
AUTHOR: GOUTFER-WURMSER F.; KONNO H.; KABURAGI Y.; OSHIDA K.; INAGAKI M.
CORPORATE SOURCE: Graduate School of Engineering, Hokkaido University, Sapporo 060-8628, Japan; Faculty of Engineering, Musashi Institute of Technology, Tokyo 158-8557, Japan; Nagano National College of Technology, Tokuma, Nagano 381-8550, Japan; Aichi Institute of Technology, Yakusa, Toyota 470-0392, Japan
SOURCE: Synthetic metals, (2001), 118(1-3), 33-38, 8 refs. ISSN: 0379-6779 CODEN: SYMEDZ
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: Switzerland
LANGUAGE: English
AVAILABILITY: INIST-18315, 354000097928480050
AN 2001-0184094 PASCAL
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AB Carbon spheres with well-dispersed nickel particles were formed by the carbonization of chelate resin complexed with Ni(II) ions at 600 and 1000°C. When the amounts of nickel after carbonization were less than I mass%, more than 90% of Ni species were paramagnetic or superparamagnetic, irrespective of carbonization temperature, indicating that they were dispersed as small clusters. For samples with 2.2-3.4 mass% Ni and formed at 600°C, most of Ni species were ferromagnetic and their **coercive** force was less than 10 Oe at 280 K. The Ni metal particles in these samples were around 10 nm in size and well dispersed, but the number density of particles was not uniform in the samples of <1 mass% Ni. For samples with 3.4 mass% Ni and formed at 1000°C, more than 80% of Ni species were ferromagnetic and the **coercive** force slightly increased to about 20 Oe. The results of XRD measurement and TEM observation showed that the Ni metal particles were around 10-30 nm and well dispersed in agreement with the magnetic properties. The results showed that the present method is promising to form the carbon materials containing well dispersed fine metal particles.

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ACCESSION NUMBER: 2001-0385445 PASCAL
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TITLE (IN ENGLISH): Tunnel splitting and quantum phase interference in biaxial ferrimagnetic particles at excited states
AUTHOR: NIE Yi-Hang; JIN Yan-Hong; LIANG J.-Q; PU F.-C
CORPORATE SOURCE: Institute of Theoretical Physics and Department of Physics, Shanxi University, Taiyuan, Shanxi 030006, China; Department of Physics, Yanbei Normal Institute, Datong, Shanxi 037000, China; Institute of Physics and Center for Condensed Matter Physics, Chinese Academy of Sciences, Beijing 100080, China; Department of Physics, Guangzhou Normal College, Guangzhou 510400, China
SOURCE: Physical review. B, Condensed matter and materials physics, (2001-10-01), 64(13), 134417-134417-7
ISSN: 1098-0121 CODEN: PRBMDO
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-144 B
AN 2001-0385445 PASCAL
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AB The tunneling splitting in biaxial ferrimagnetic particles at excited states with an explicit calculation of the prefactor of exponent is obtained in terms of periodic instantons that are responsible for tunneling at excited states and is shown as a function of magnetic field applied along an arbitrary direction in the plane of hard and medium axes. Using **complex** time path integral we demonstrate the oscillation of tunnel splitting with respect to the **magnitude** and the direction of the magnetic field due to the quantum phase interference of two tunneling paths of opposite windings. The oscillation is gradually smeared and in the end the tunnel splitting monotonously increases with the **magnitude** of the magnetic field when the direction of the magnetic field tends to the medium axis. The oscillation behavior is similar to the recent experimental observation with Fe.sub.8 molecular clusters. A candidate of possible experiments to observe the effect of quantum phase interference in the ferrimagnetic particles is proposed.

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ACCESSION NUMBER: 2001-0182542 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2001 American Institute of Physics. All rights reserved.
TITLE (IN ENGLISH): Magnetic anisotropy of fcc transition-metal clusters: Role of surface relaxation
AUTHOR: GUIRADO LOPEZ R.
CORPORATE SOURCE: Instituto de Fisica Manuel Sandoval Vallarta, Universidad Autonoma de San Luis Potosi, 78000 San Luis Potosi, Mexico
SOURCE: Physical review. B, Condensed matter and materials physics, (2001-05-01), 63(17), 174420-174420-9
ISSN: 1098-0121 CODEN: PRBMDO
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-144 B
AN 2001-0182542 PASCAL
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AB The magnetic-anisotropy energy (MAE) of fcc transition-metal (TM) clusters (19<=N<=79) is determined using two different semiempirical schemes. First within a tight-binding calculation for the d band, the equilibrium geometries of the clusters, which are built by adding successive atomic shells around a central atom, are obtained by means of the fictitious Lagrangian method introduced by Car and Parrinello [Phys. Rev. Lett. 55, 2471 (1985); 60, 204 (1988)]. In this approach, both atomic and electronic structures are treated simultaneously in the minimization algorithm, a procedure that reveals the existence of a highly nonuniform relaxation profile of the intershell spacings in the clusters, which may contract as well as expand, in agreement with the results found at surfaces of TM<right single quotation mark>s. In a second step, treating the spin-orbit coupling nonperturbatively and also within the framework of a d-band Hamiltonian, we analyze the role of this **complex** interlayer-spacing distribution on the magnetoanisotropic behavior of the clusters. In all cases, we perform single-point energy calculations, for two different directions of the magnetization δ, on the previously optimized geometries using the Car-Parrinello method. The MAE shows a complicated behavior as a function of cluster size, bond length, and d-band filling. Moreover, by investigating different relaxations, it is shown that the existence of this nonuniform pattern of interatomic distances causes appreciable changes in the **magnitude** of the MAE and can be also at the origin of reorientations of the magnetization in the particles. We conclude that this kind of structural transformations are essential for quantitative predictions of the MAE in cluster systems.

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ACCESSION NUMBER: 2000-0369523 PASCAL
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TITLE (IN ENGLISH): Deviation from the superparamagnetic behaviour of fine-particle systems
AUTHOR: MALAESCU I.; MARIN C. N.
CORPORATE SOURCE: Faculty of Physics, West University of Timisoara, Bd. V.Parvan # 4, Timisoara 1900, Romania
SOURCE: Journal of magnetism and magnetic materials, (2000), 218(1), 91-96, 21 refs.
ISSN: 0304-8853 CODEN: JMMMDC
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: Netherlands
LANGUAGE: English
AVAILABILITY: INIST-17230, 354000090736940140

AN 2000-0369523 PASCAL
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AB Studies concerning superparamagnetic behaviour of fine **magnetic particle** systems were performed using static and radiofrequency measurements, in the range 1-60 MHz. The samples were: a ferrofluid with magnetite particles dispersed in kerosene (sample A), magnetite powder (sample B) and the same magnetite powder dispersed in a polymer (sample C). Radiofrequency measurements indicated a maximum in the imaginary part of the **complex** magnetic susceptibility, for each of the samples, at frequencies with the **magnitude** order of tens of MHz, the origin of which was assigned to Neel-type relaxation processes. The static measurements showed a Langevin-type dependence of magnetisation M and of susceptibility X, on the magnetic field for sample A. For samples B and C deviations from this type of dependence were found. These deviations were analysed qualitatively and explained in terms of the interparticle interactions, dispersion medium influence and surface effects.

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ACCESSION NUMBER: 2000-0392515 PASCAL
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TITLE (IN ENGLISH): Micromagnetic modelling : the current state of the art
AUTHOR: FIDLER J.; SCHREFL T.
CORPORATE SOURCE: Institute of Applied and Technical Physics, Vienna University of Technology, Wiedner Hauptstr. 8-10/137, 1040 Vienna, Austria
SOURCE: Journal of physics. D. Applied physics, (2000), 33(15), R135-R156, refs. 2 p.1/4
ISSN: 0022-3727 CODEN: JPAPBE
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United Kingdom
LANGUAGE: English
AVAILABILITY: INIST-5841, 354000090235330020

AN 2000-0392515 PASCAL
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AB The increasing information density in magnetic recording, the miniaturization in magnetic sensor technology, the trend towards nanocrystalline magnetic materials and the improved availability of large-scale computer power are the main reasons why micromagnetic modelling has been developing extremely rapidly. Computational micromagnetism leads to a deeper understanding of hysteresis effects by visualization of the magnetization reversal process. Recent advances in numerical simulation techniques are reviewed. Higher order finite elements and adaptive meshing have been introduced, in order to reduce the discretization error. The use of a hybrid boundary/finite element method enables accurate stray field computation for arbitrary shaped particles and takes into account the granular microstructure of the material. A dynamic micromagnetic code based on the Gilbert equation of motion to study the time evolution of the magnetization has been developed. Finite element models for different materials and magnet shapes are obtained from a Voronoi construction and subsequent meshing of the polyhedral regions. Adaptive refinement and coarsening of the finite element mesh guarantees accurate solutions near magnetic inhomogeneities or domain walls, while keeping the number of elements small. The polycrystalline microstructure and assumed random magnetocrystalline anisotropy of elongated Co elements decreases the **coercive** field and the switching time compared to zero anisotropy elements, in which vortices form and move only after a certain waiting time after the application of a reversed field close to the **coercive** field.
NiFe elements with flat, rounded and slanted ends show different hysteresis properties and switching dynamics. Micromagnetic simulations show that the magnetic properties of intergranular regions in nucleation-controlled Nd-Fe-B hard magnetic materials control the **coercive** field. Exchange interactions between neighbouring soft and hard grains lead to remanence enhancement of isotropically oriented grains in nanocrystalline composite magnets. Upper limits of the **coercive** field of pinning-controlled Sm-Co magnets for high-temperature applications are predicted from the micromagnetic calculations. Incorporating thermally activated magnetization reversal and micromagnetics we found **complex** magnetization reversal mechanisms for small spherical **magnetic particles**.
The magnetocrystalline anisotropy and the external field strength determine the switching mechanism. Three different regimes have been identified. For fields, which are smaller than the anisotropy field, magnetization by coherent switching has been observed. Single droplet nucleation occurs, if the external field is comparable to the anisotropy field, and multi-droplet nucleation is the driving reversal process for higher fields.

on STN
ACCESSION NUMBER: 1999-0183582 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 1999 American Institute of Physics. All rights reserved.
TITLE (IN ENGLISH): Comparison of magnetostatic field calculation methods on two-dimensional square grids as applied to a micromagnetic standard problem
AUTHOR: MCMICHAEL R. D.; DONAHUE M. J.; PORTER D. G.; EICKE Jason
CORPORATE SOURCE: National Institute of Standards and Technology, Gaithersburg, Maryland 20899; Institute for Magnetics Research, George Washington University, Washington, DC 20052
SOURCE: Journal of applied physics, (1999-04-15), 85(8), 5816-5818
ISSN: 0021-8979 CODEN: JAPIAU
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-126
AN 1999-0183582 PASCAL
CP Copyright .COPYRGT. 1999 American Institute of Physics. All rights reserved.
AB Magnetization reversal modes and coercivities were calculated for a **magnetic particle** with thickness : width : length aspect ratios 0.1 : 1 : 5 as a function of the reduced particle width d/l.sub.e.sub.x, where d is the particle width and l.sub.e.sub.x is the intrinsic magnetostatic exchange length. With only exchange energy and magnetostatic energy included, the particle corresponds to μMAG standard problem Number 2. The problem is modeled with two-dimensional grids of three-dimensional spins, and the results are compared for two methods of calculating magnetostatic energies, the constant magnetization method and the constant charge method. For both magnetostatic computational methods, the coercivity decreases from H.sub.c/M.sub.s=0.06±0.003 to 0.014±0.003 over the range 3<d/l.sub.e.sub.x<80, where the uncertainties reflect the field step size. Also over this interval, as d/l.sub.e.sub.x increases, the magnetization exhibits three modes of reversal: nearly uniform rotation, transverse switching of end domains followed by propagation of head-to-head domain walls from the ends to the center of the particle, and nucleation and propagation of vortices accompanied by more **complex** domain structures. .COPYRGT. 1999 American Institute of Physics.

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on STN
ACCESSION NUMBER: 1999-0059344 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 1999 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): Computation of the transition from the soft to the hard magnetic state by varying the anisotropy constant of nanoscaled Nd.sub.2Fe.sub.1.sub.4B
AUTHOR: FISCHER R.; KRONMUELLER H.
CORPORATE SOURCE: Max-Planck-Institut fuer Metallforschung, 70569 Stuttgart, Germany, Federal Republic of
SOURCE: Journal of magnetism and magnetic materials, (1999), 191(1-2), 181-188, 25 refs.
ISSN: 0304-8853 CODEN: JMMMDC
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: Netherlands
LANGUAGE: English
AVAILABILITY: INIST-17230, 354000073460500250

AN 1999-0059344 PASCAL

AB Computational micromagnetism can provide us with a more detailed understanding of magnetization processes in nanostructured ferromagnetic materials. In particular, it is possible to simulate the transition from the soft to the hard magnetic state by varying only the magnetocrystalline anisotropy and keeping all other conditions constant. The computation of the remanence J.sub.r as a function of the first anisotropy constant K.sub.1 (K.sub.2 K.sub.1/5) leads to a curve with a maximum. As expected the remanence is approximately zero for the soft magnetic case with small K.sub.1. Here the magnetization distribution is mainly determined by the competitive effects of the short-range exchange interactions and the long-range stray fields. This finally leads to magnetic vortex states. But with increasing K .sub.1 the magnetic moments are preferably oriented along certain easy axes causing a rapid increase of the remanence. Now the magnetization distribution is determined by the competitive effects of the local anisotropy and the short-range exchange interaction. The maximum of the J.sub.r(K.sub.1) curve is therefore positioned at K.sub.1 values, where the range of the exchange interaction δ.sub.B = $\pi\sqrt{A}$/K.sub.1 is in order of about 1/4-1/2 of the mean grain diameter. A further increase of K.sub.1 finally suppresses the intergranular exchange interactions. Now only the magnetocrystalline anisotropy determines the magnetization distribution and the remanence decreases to the value for an ensemble of isolated grains. The computation of the coercivity H.sub.c as a function of the anisotropy constant K.sub.1 leads to an approximately linear increase of the coercivity with increasing anisotropy K.sub.1. Therefore, the Stoner-Wohlfarth theory of an ideal **magnetic particle** explains also the H.sub.c(K.sub.1) dependence of **complex** grain arrangements. Small deviations only exist for the soft magnetic case, where the Stoner-Wohlfarth theory fails.